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Weiner et al.

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(54) **NUCLEIC ACID MOLECULES ENCODING NOVEL HERPES ANTIGENS, VACCINE COMPRISING THE SAME, AND METHODS OF USE THEREOF**

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(65) **Prior Publication Data**

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Related U.S. Application Data

(62) Division of application No. 13/982,457, filed as application No. PCT/US2012/023398 on Jan. 31, 2012, now Pat. No. 9,243,041.

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(51) **Int. Cl.**

C07K 14/005 (2006.01)
C12N 7/00 (2006.01)
A61K 39/12 (2006.01)
A61K 39/245 (2006.01)
A61K 39/00 (2006.01)
A61K 39/25 (2006.01)

(52) **U.S. Cl.**

CPC **C07K 14/005** (2013.01); **A61K 39/12** (2013.01); **A61K 39/245** (2013.01); **A61K 39/25** (2013.01); **C12N 7/00** (2013.01); **A61K 2039/53** (2013.01); **C12N 2710/16011** (2013.01); **C12N 2710/16111** (2013.01); **C12N 2710/16122** (2013.01); **C12N 2710/16134** (2013.01); **C12N 2710/16622** (2013.01); **C12N 2710/16634** (2013.01); **C12N 2710/16722** (2013.01); **C12N 2710/16734** (2013.01)

(58) **Field of Classification Search**

CPC C12N 7/00; C12N 15/86; C12N 2710/16034; C12N 2710/16734; C12N 15/869; C12N 2710/16762; A61K 39/12; A61K 39/245; A61K 2039/525; A61K 2039/6075; A61K 39/25; A61K 39/42; A61K 35/763; C07K 14/005; C07K 14/03; C07K 14/035; C07K 16/085

See application file for complete search history.

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(57) **ABSTRACT**

Provided herein are nucleic acid sequences that encode novel consensus amino acid sequences of herpes virus antigens, as well as genetic constructs/vectors and vaccines expressing the sequences. Also provide herein are methods for generating an immune response against herpes virus using the vaccines that are provided.

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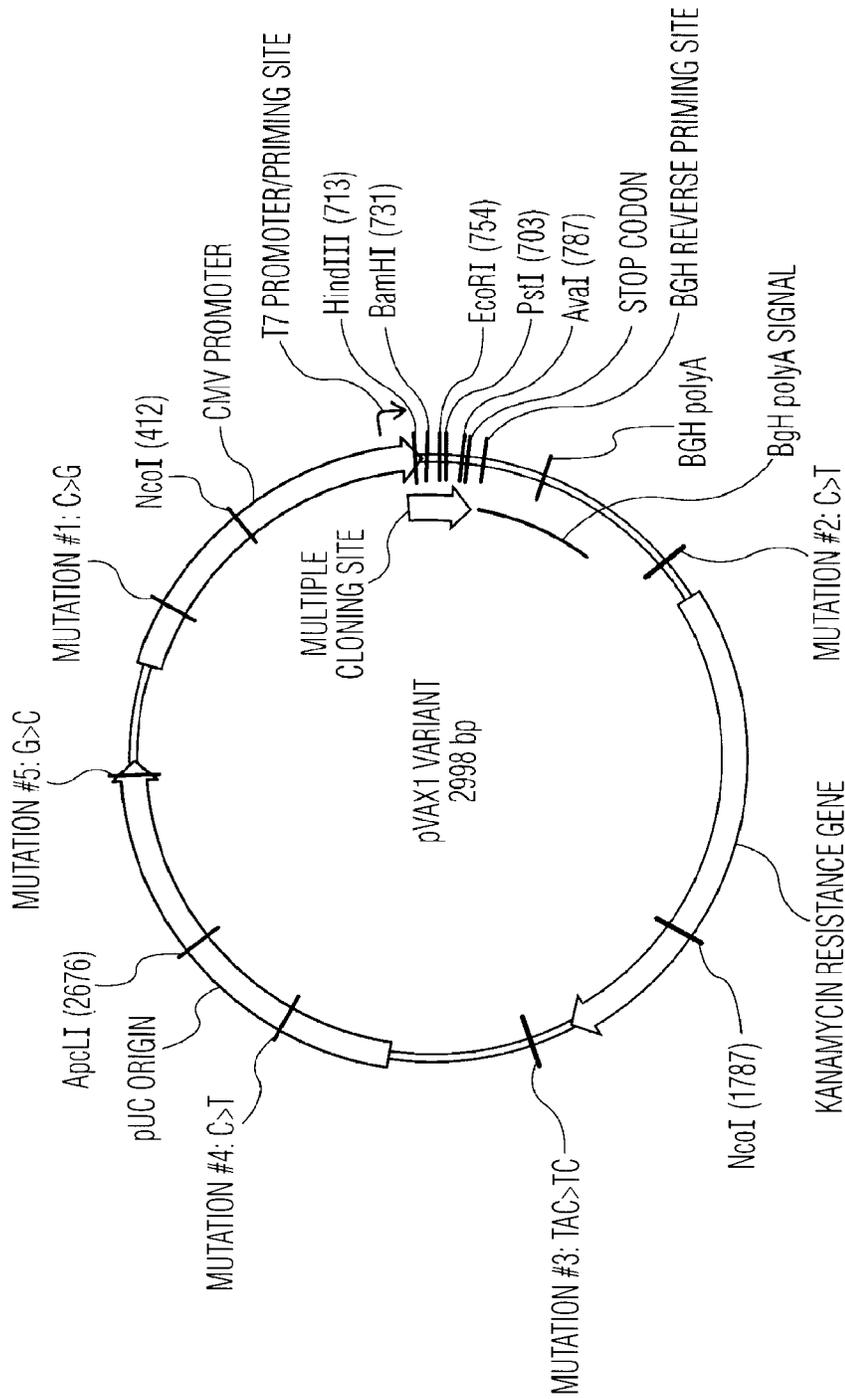


FIG. 1

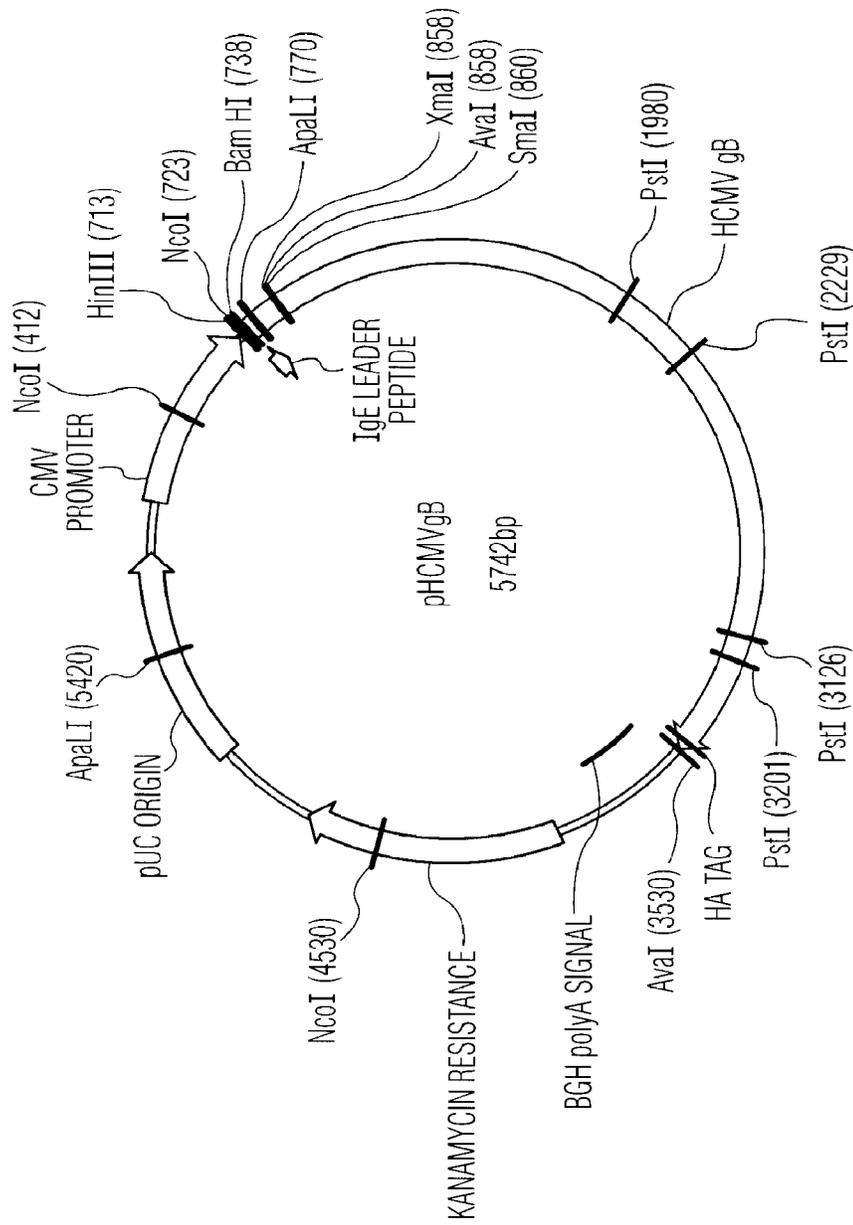


FIG. 2

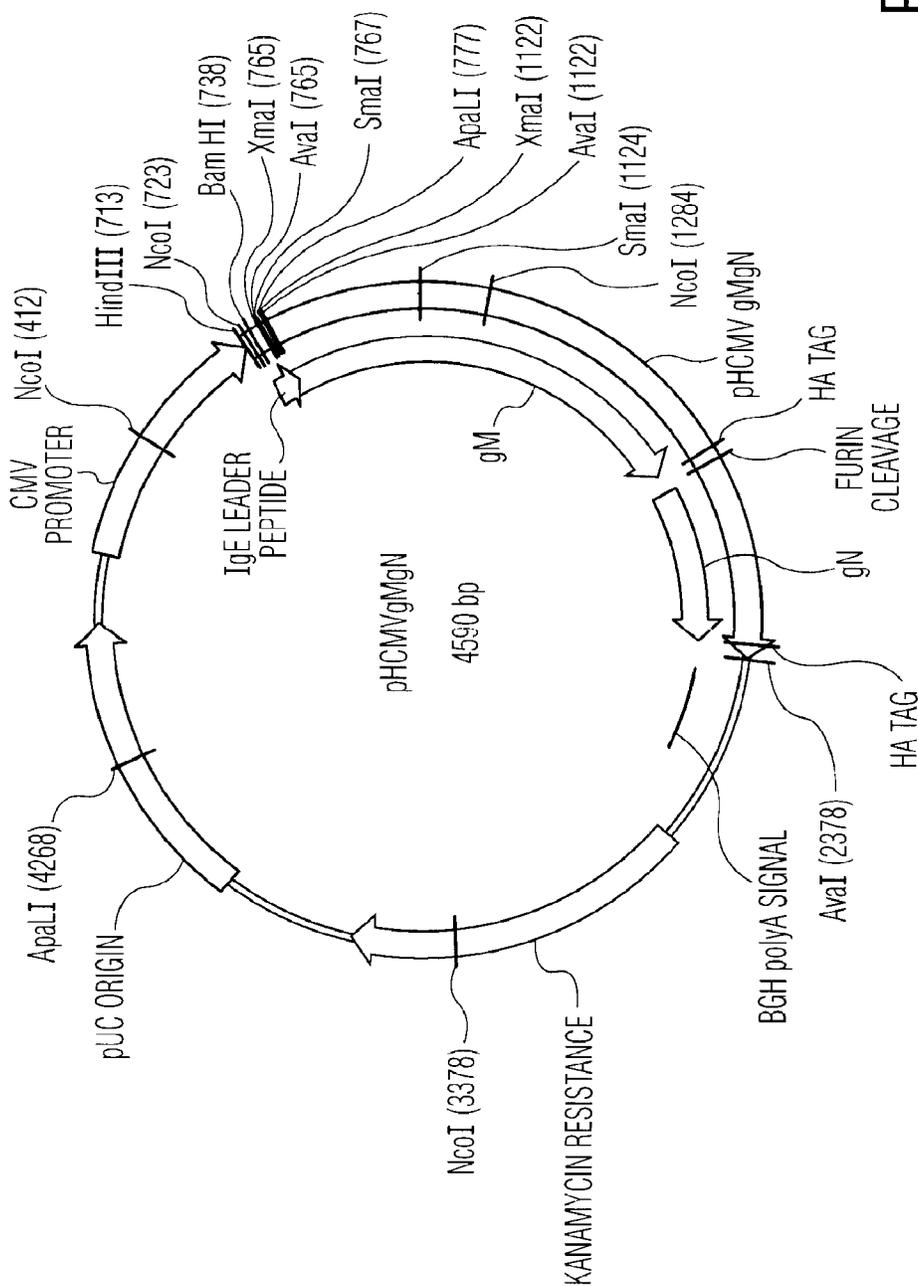


FIG. 3

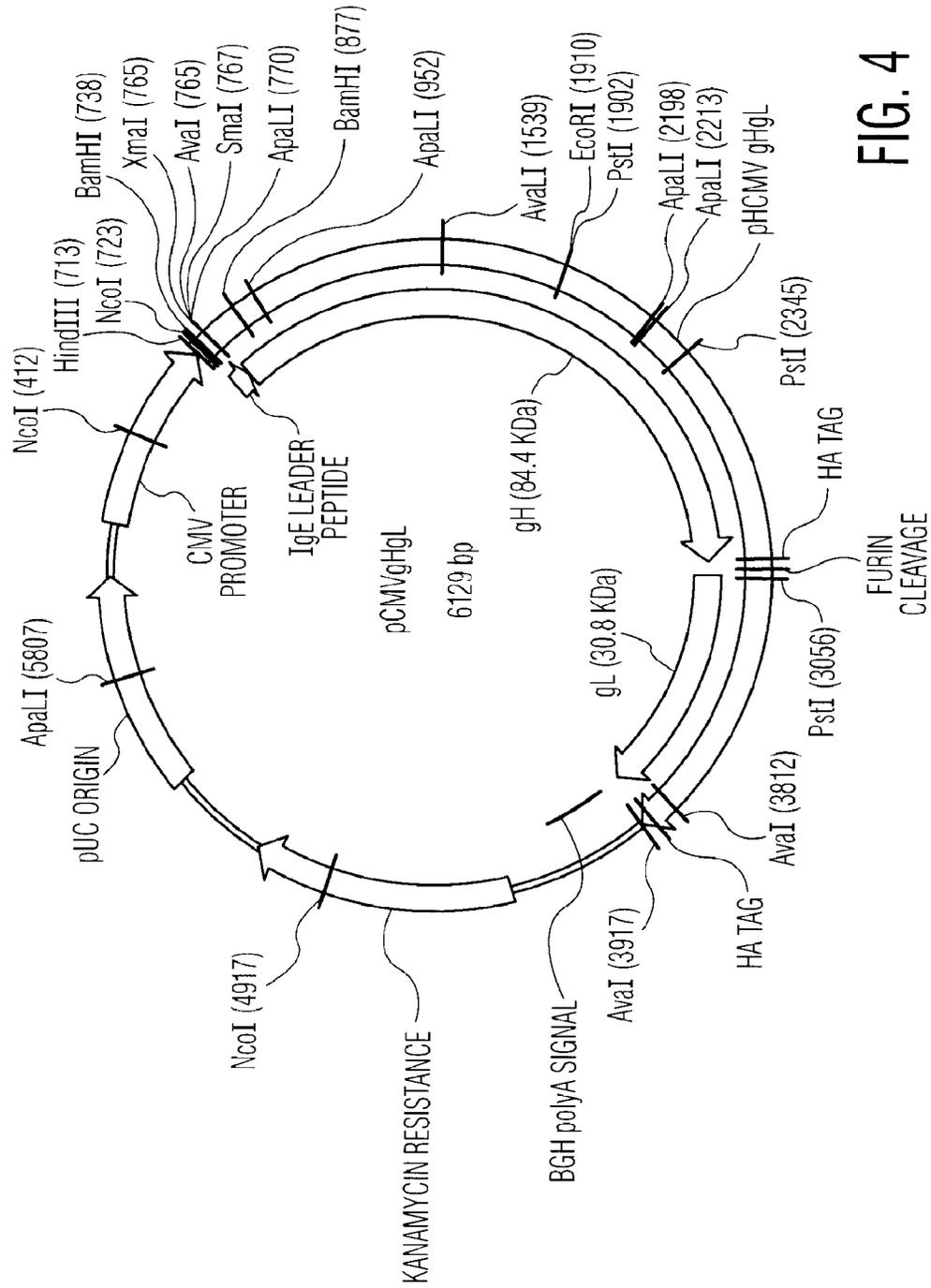


FIG. 4

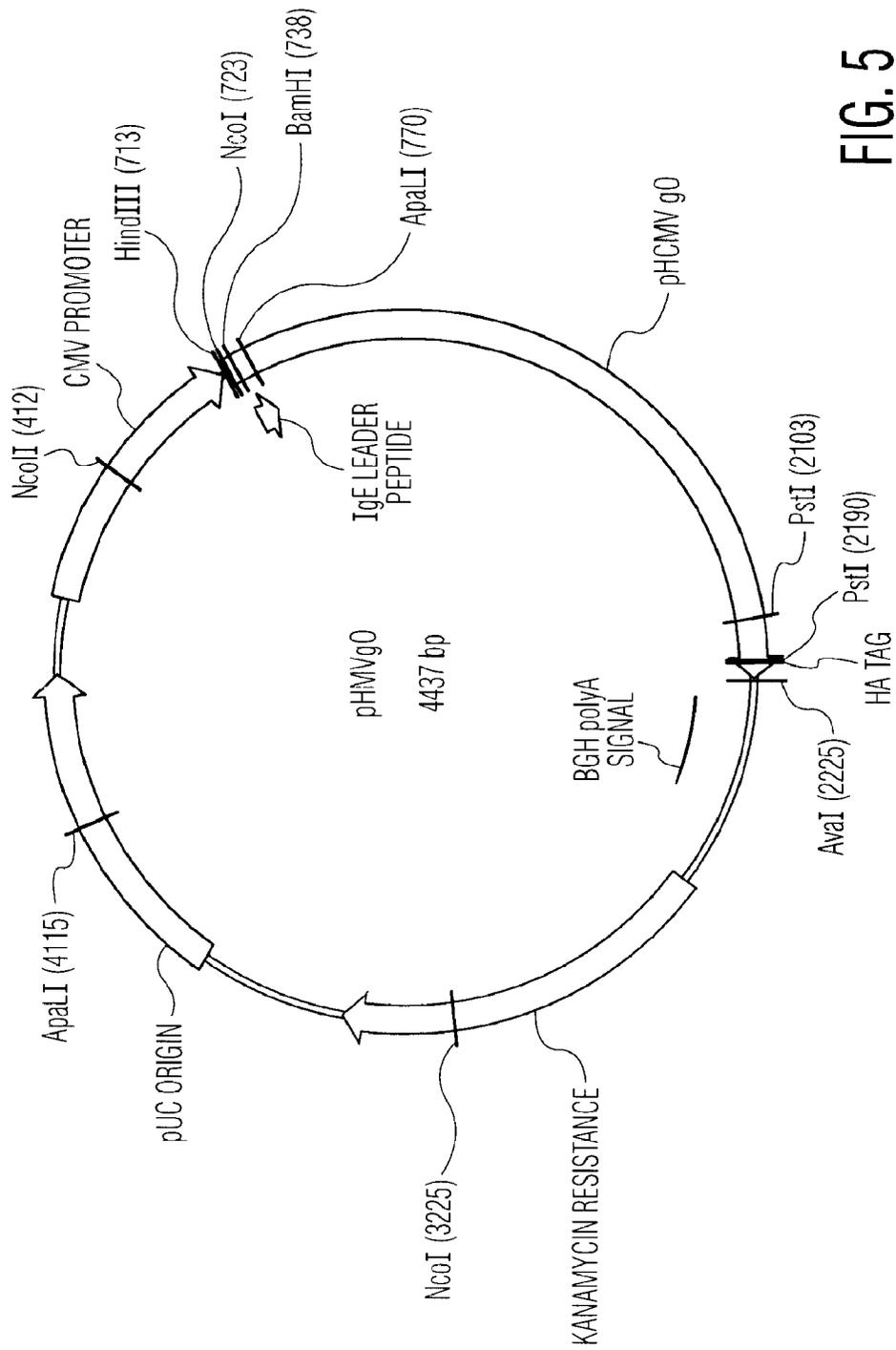


FIG. 5

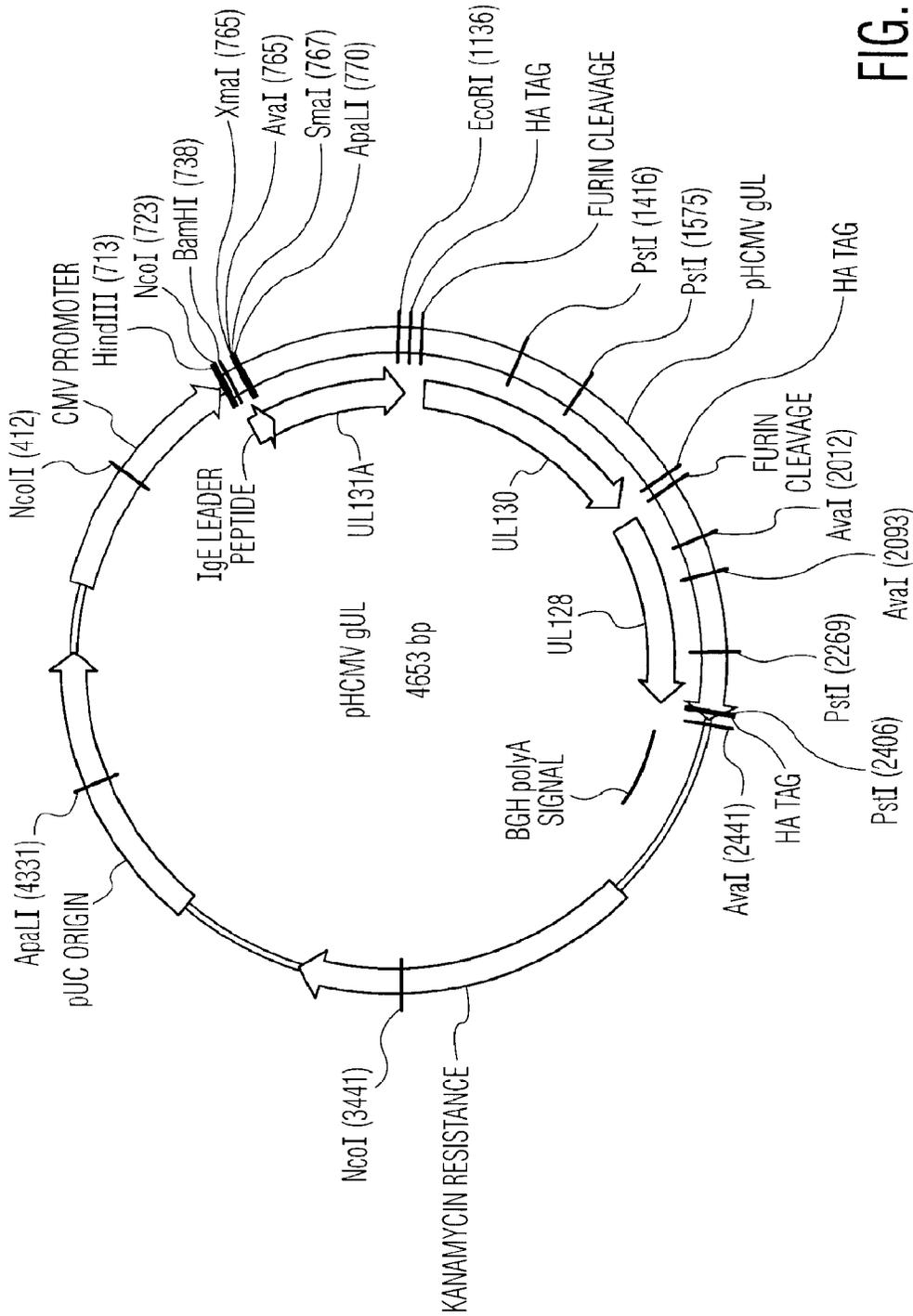


FIG. 6

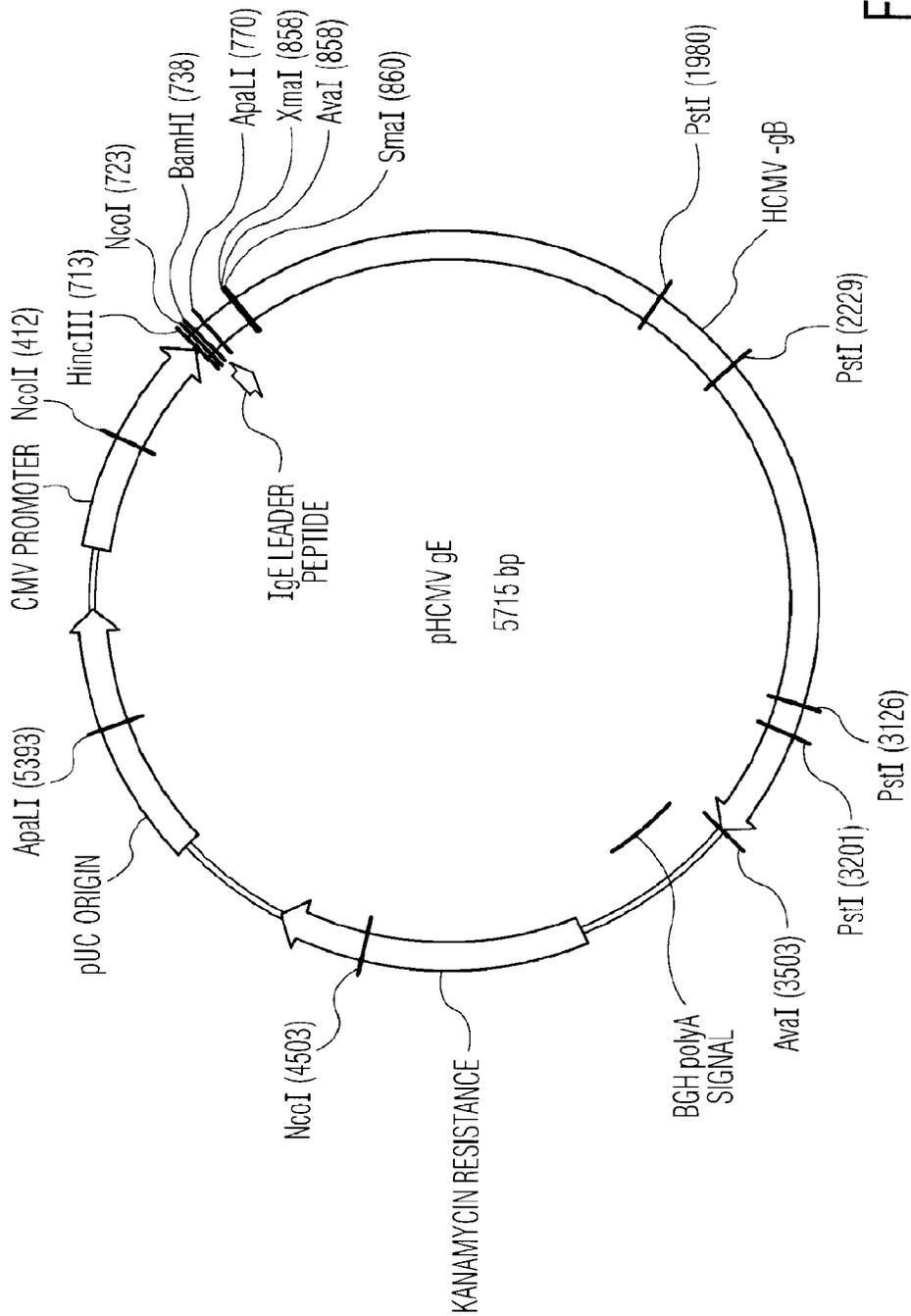


FIG. 7

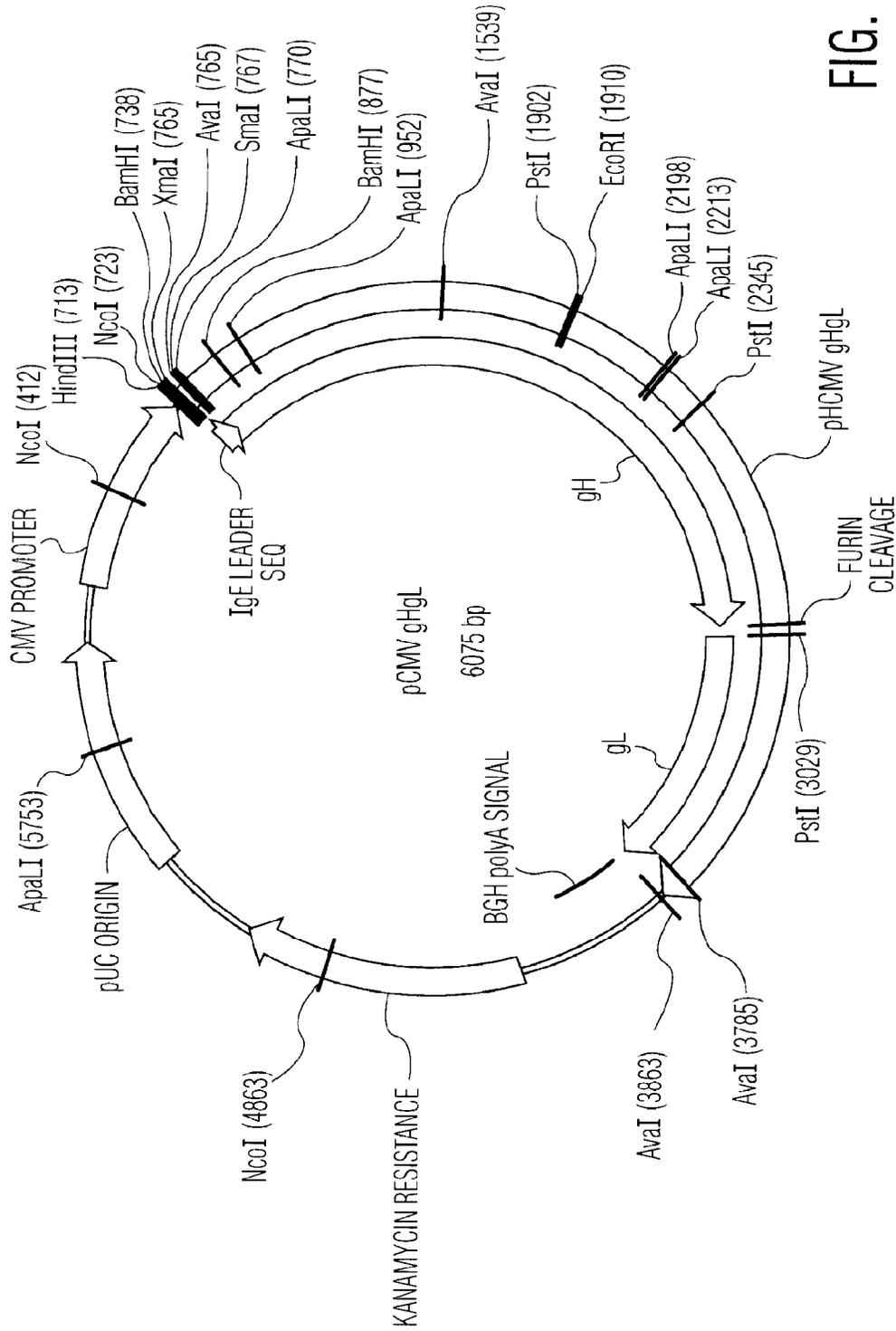


FIG. 8

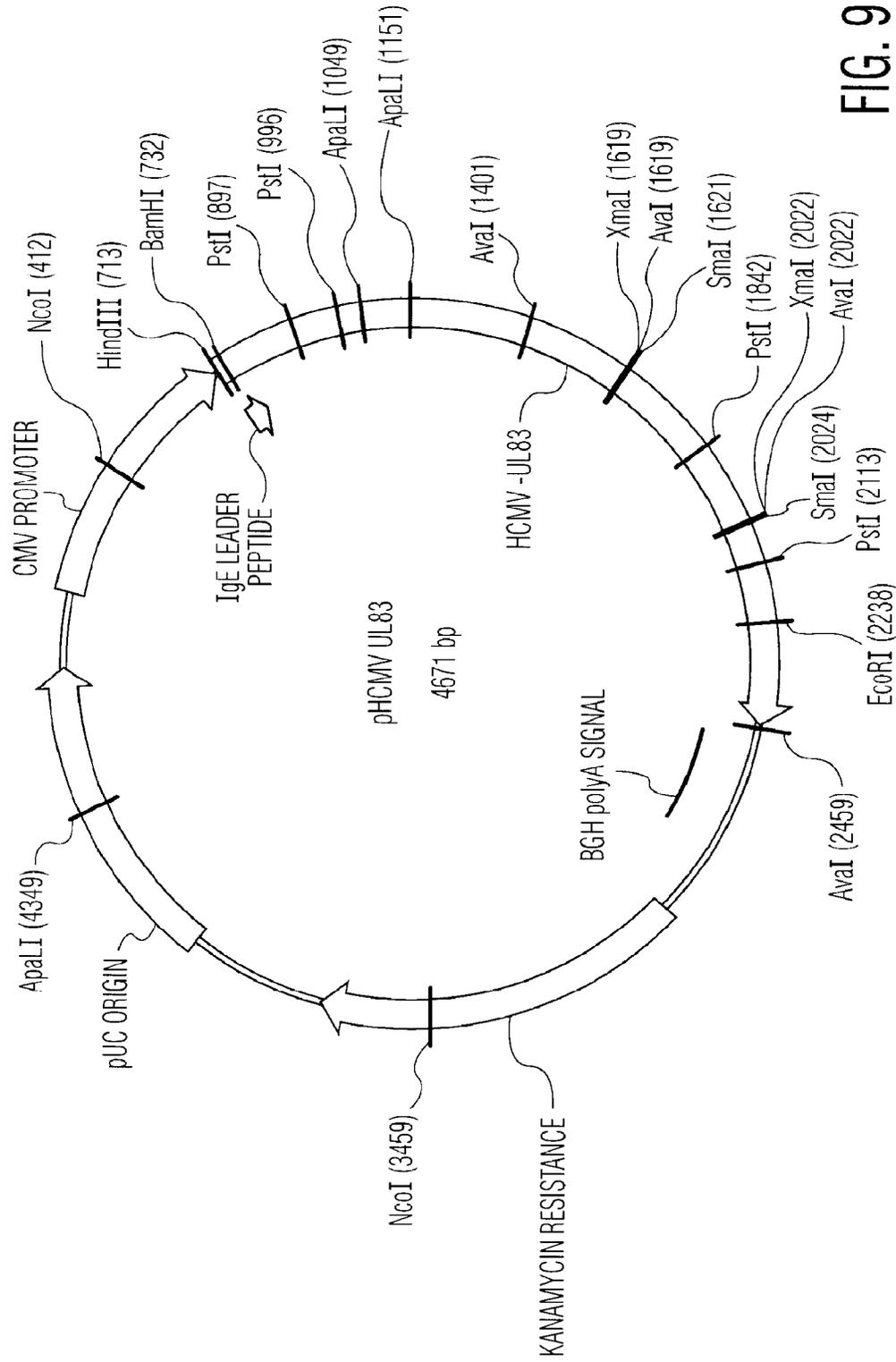


FIG. 9

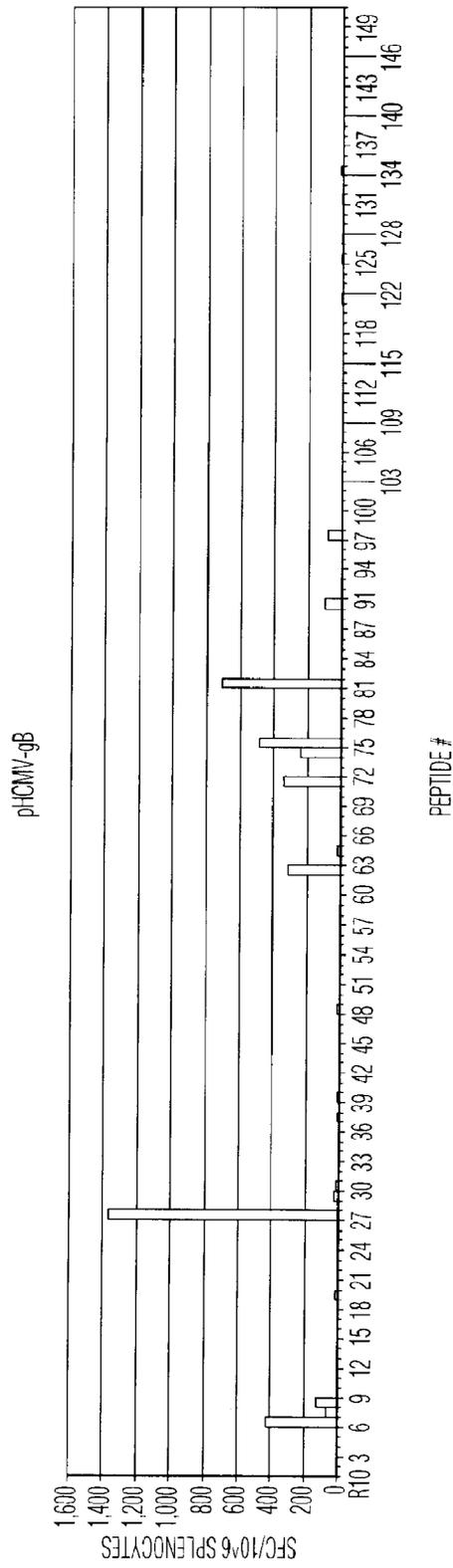


FIG. 10

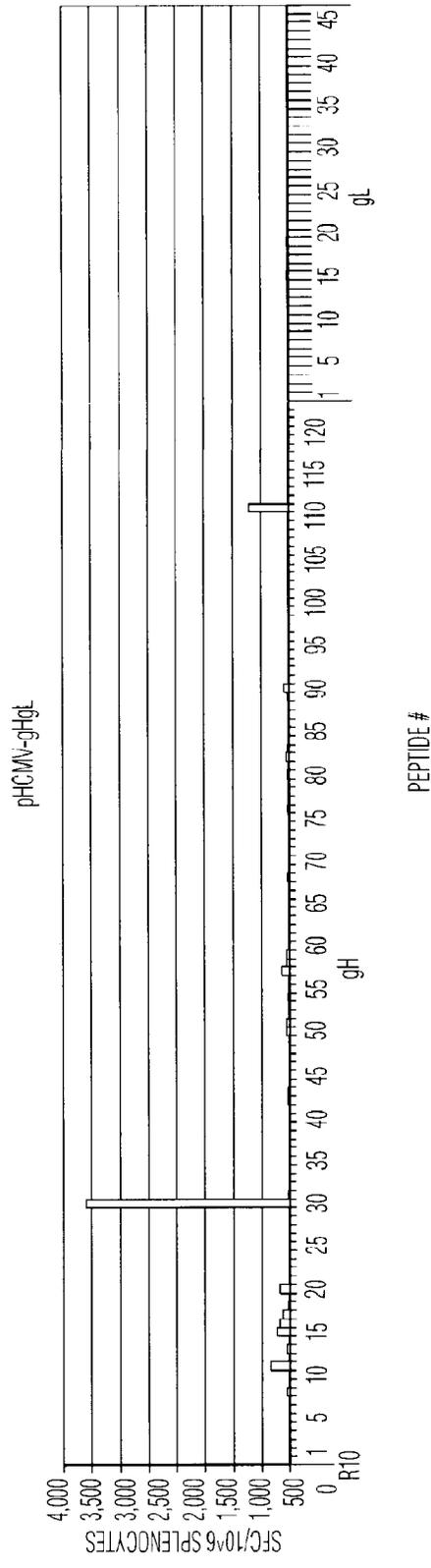


FIG. 11

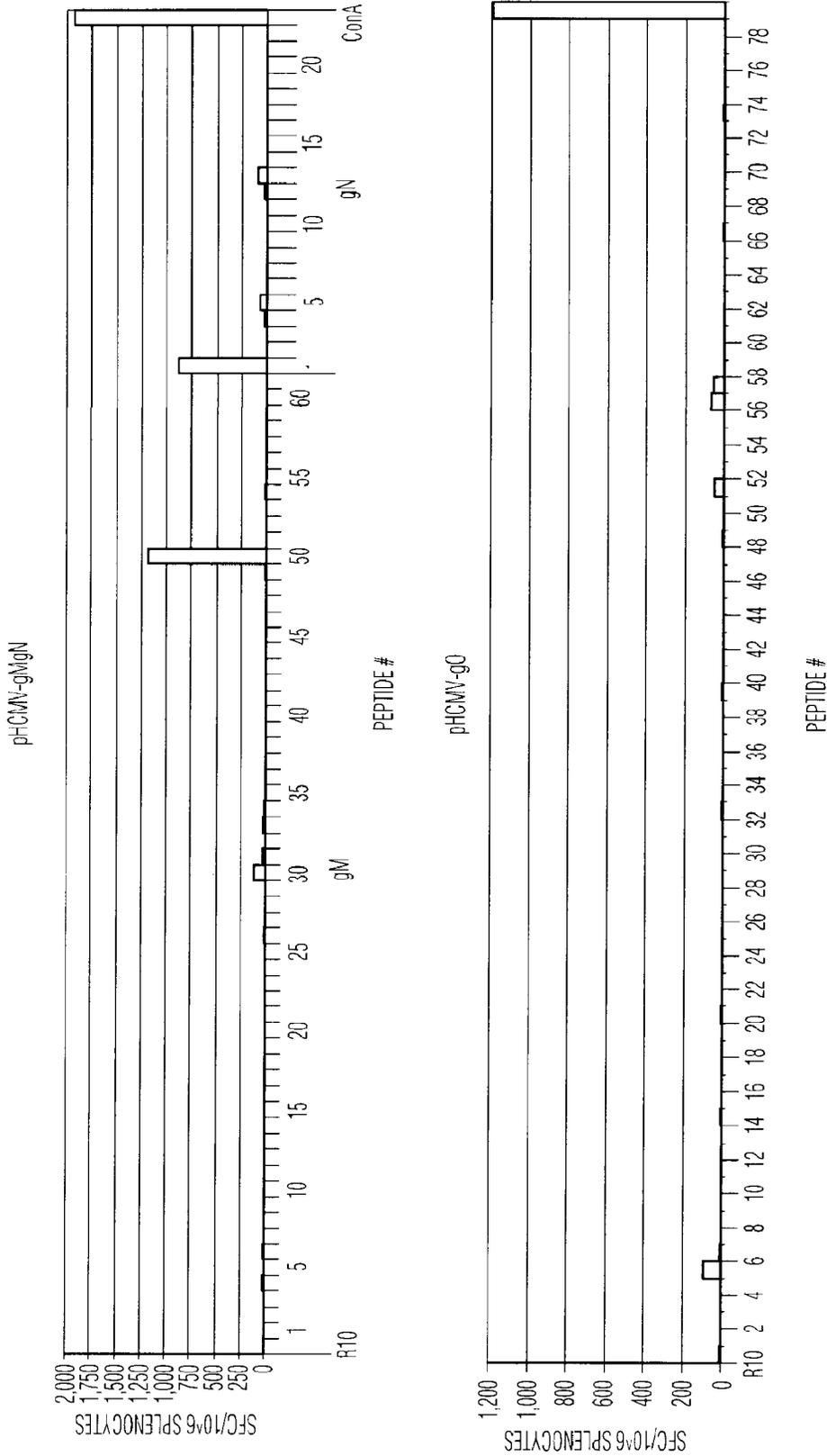


FIG. 12

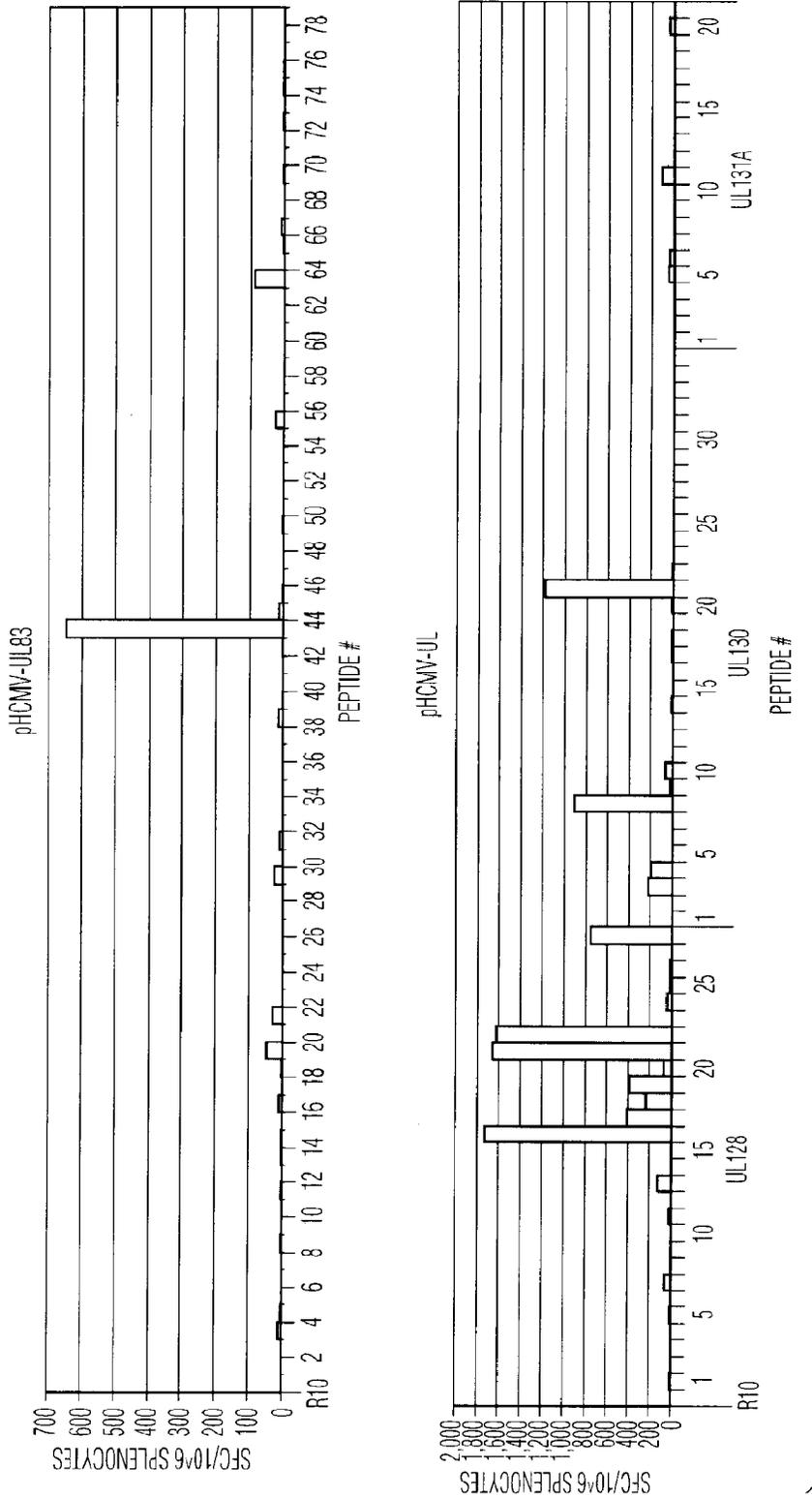


FIG. 13

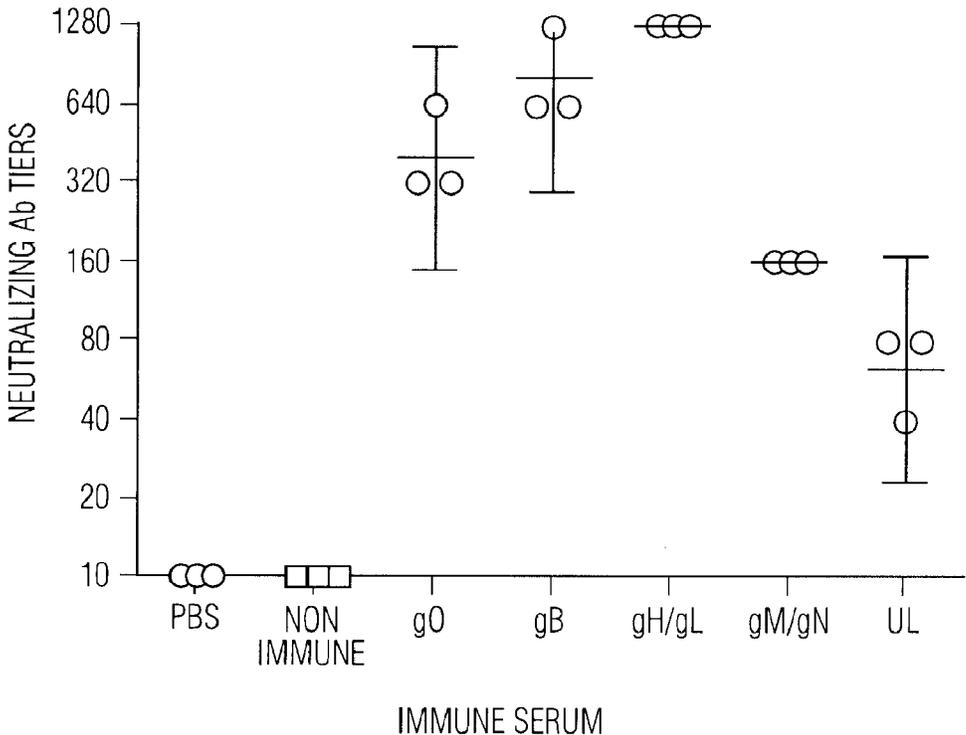


FIG. 14

	pHCMV-		Ag	ELISpot T cell Epitopes (B6)				B cell responses		Vaccine
				Total	Dom #	Subdom #	#	ELISA (1:x)	Neut Titr	
1	gB	gB	3,300	1	1,400	4	1,900	1,350	650	Y
2	gH-gL	gH gL	4,900	1	3,600	3	1,300	4,500 4,500	1,280	Y
3	gM-gN	gM gN	2,325	1	1,200	1	125		160	N
4	gO	gO	200	1	900	2	100			Y
5	gUL	UL128 UL130 UL131A	6,900	2	3,300	2	1,200		50	Y
6	gUL83	gUL83	800	1	650	2	150		?	Maybe

FIG. 15

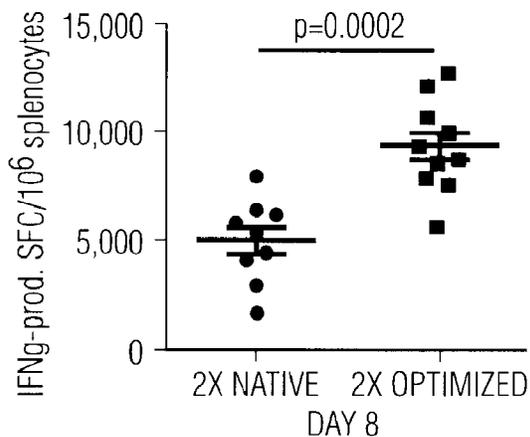


FIG. 16a

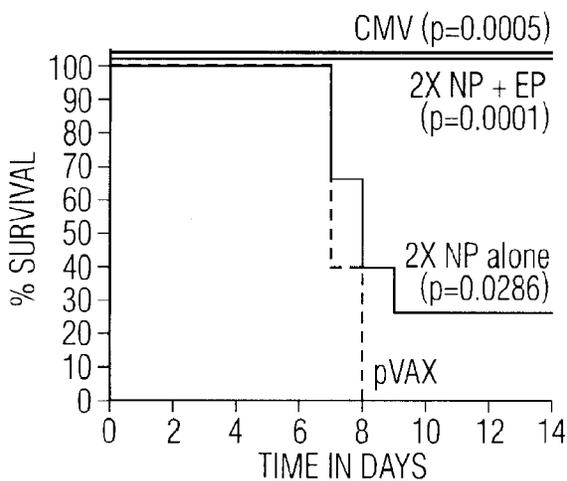


FIG. 16b

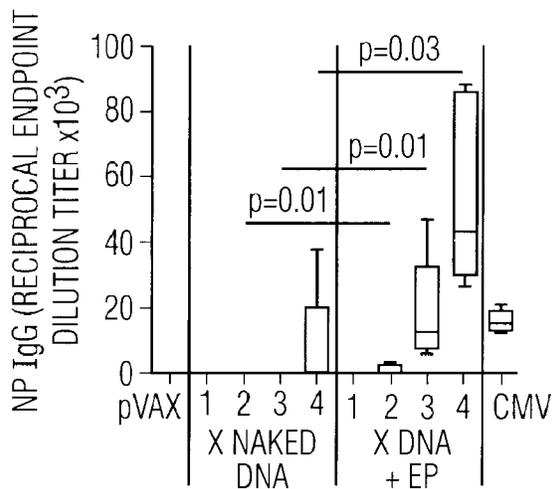


FIG. 16c

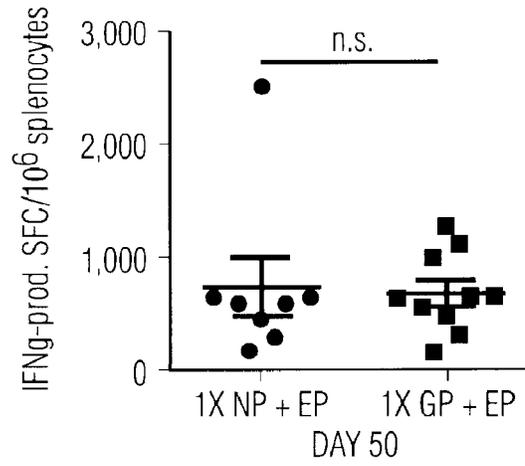


FIG. 16d

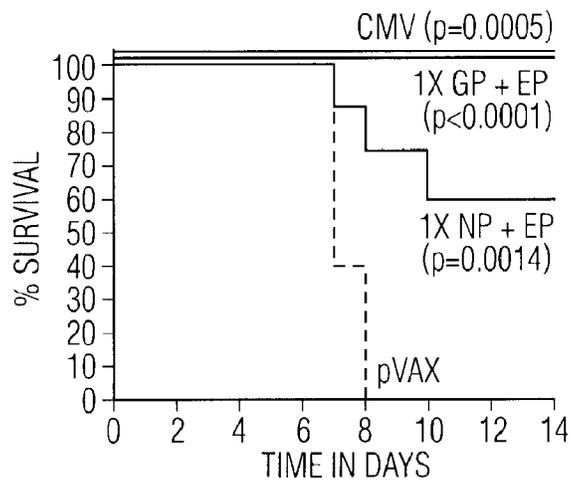


FIG. 16e

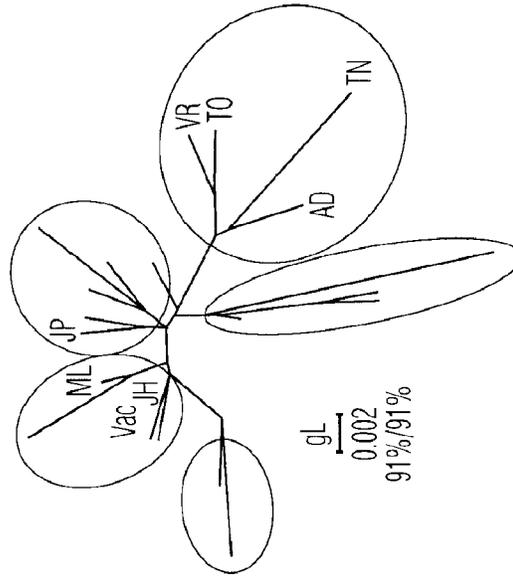


FIG. 17c

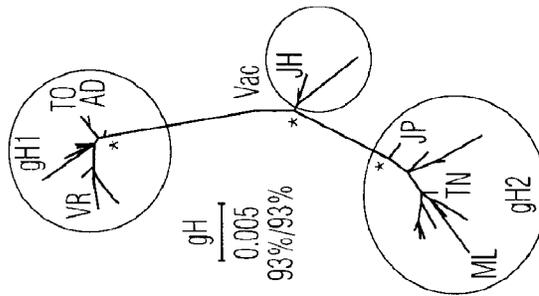


FIG. 17b

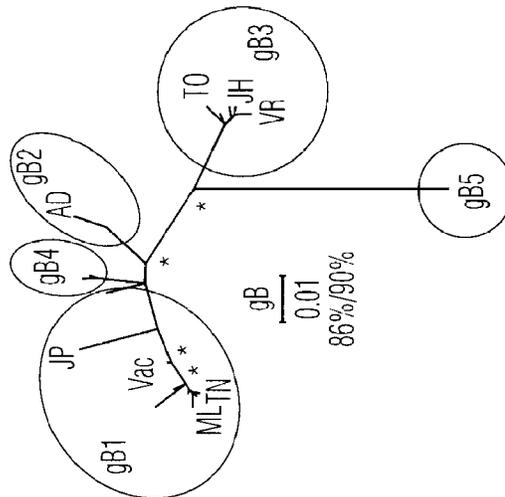


FIG. 17a

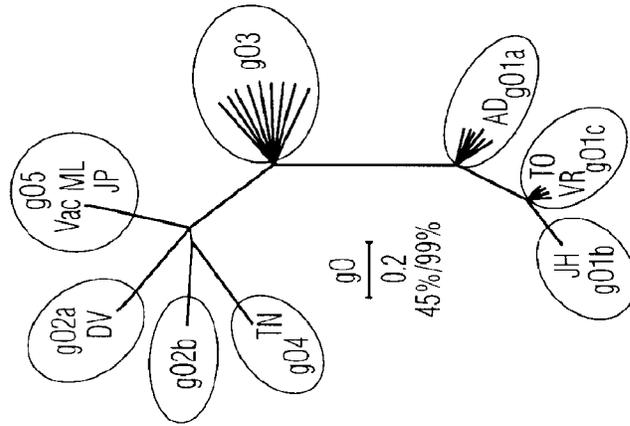


FIG. 17f

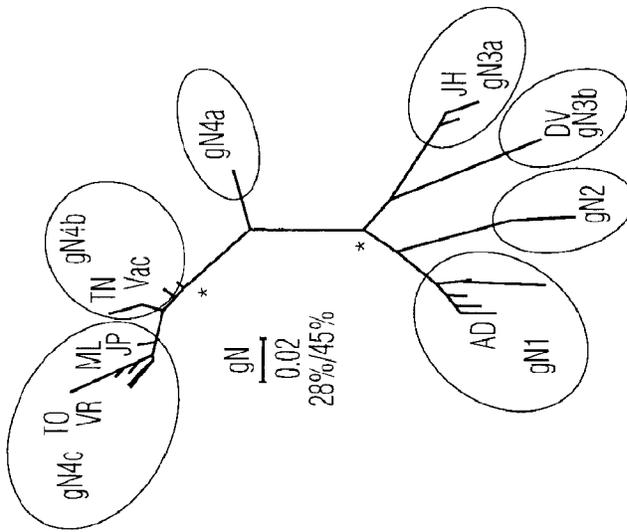


FIG. 17e

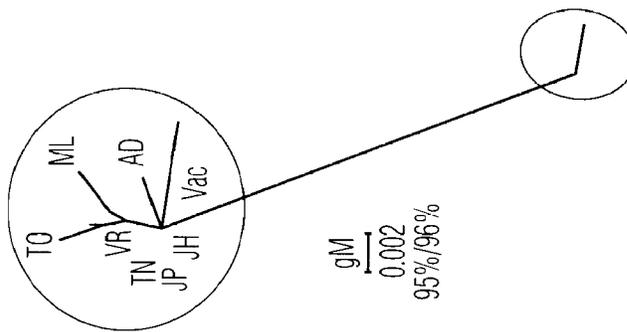


FIG. 17d

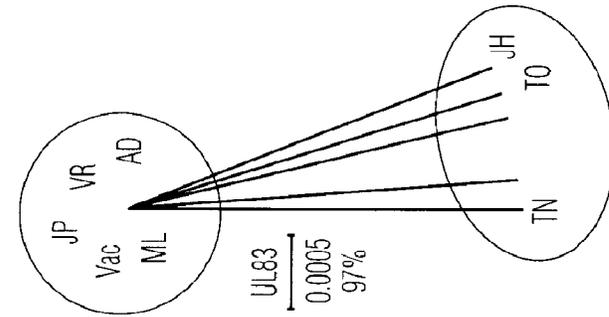


FIG. 17j

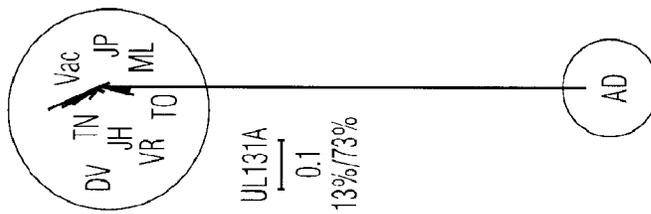


FIG. 17i

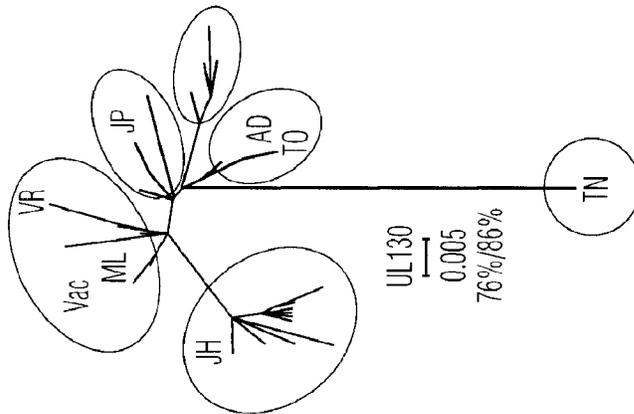


FIG. 17h

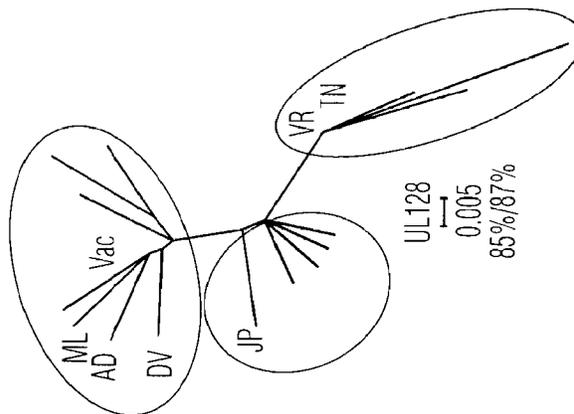


FIG. 17g

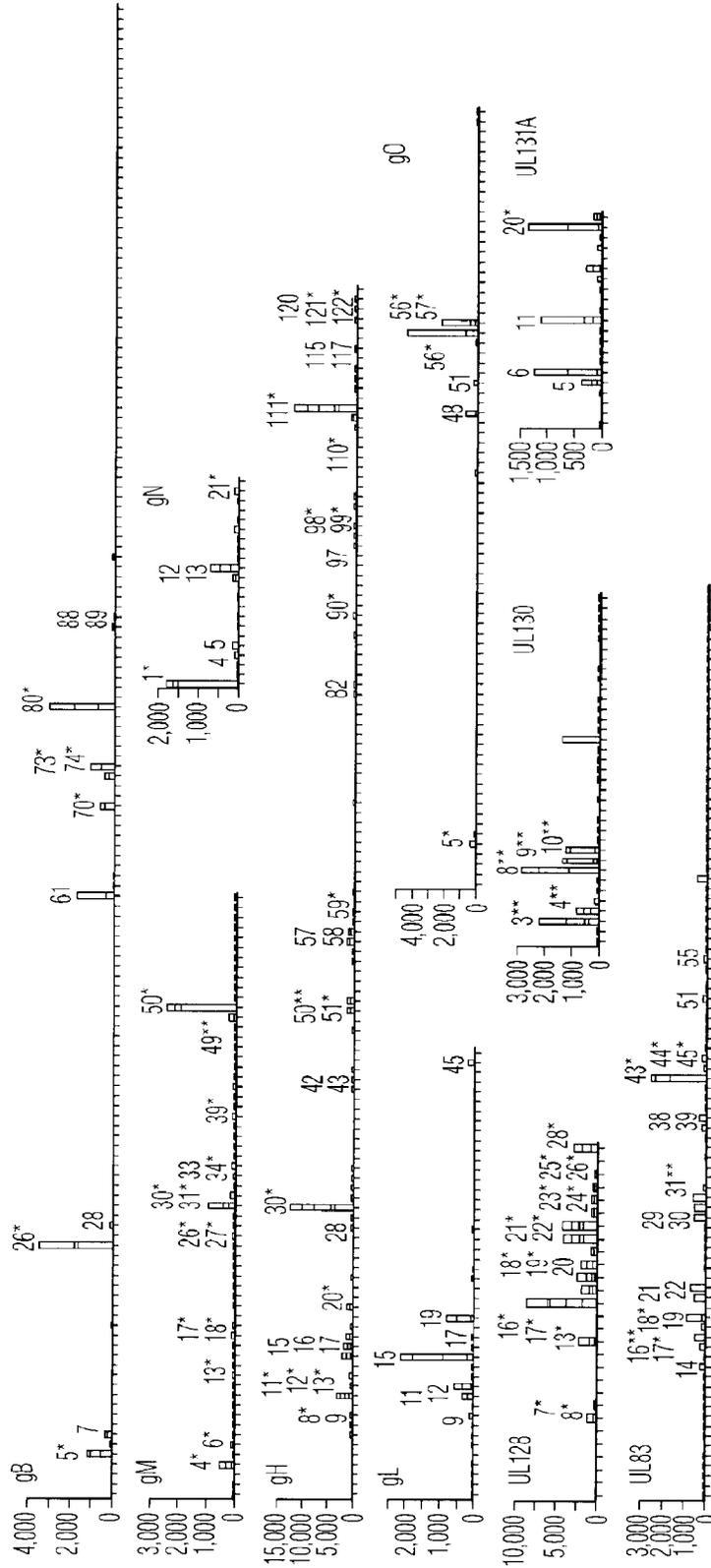


FIG. 18a

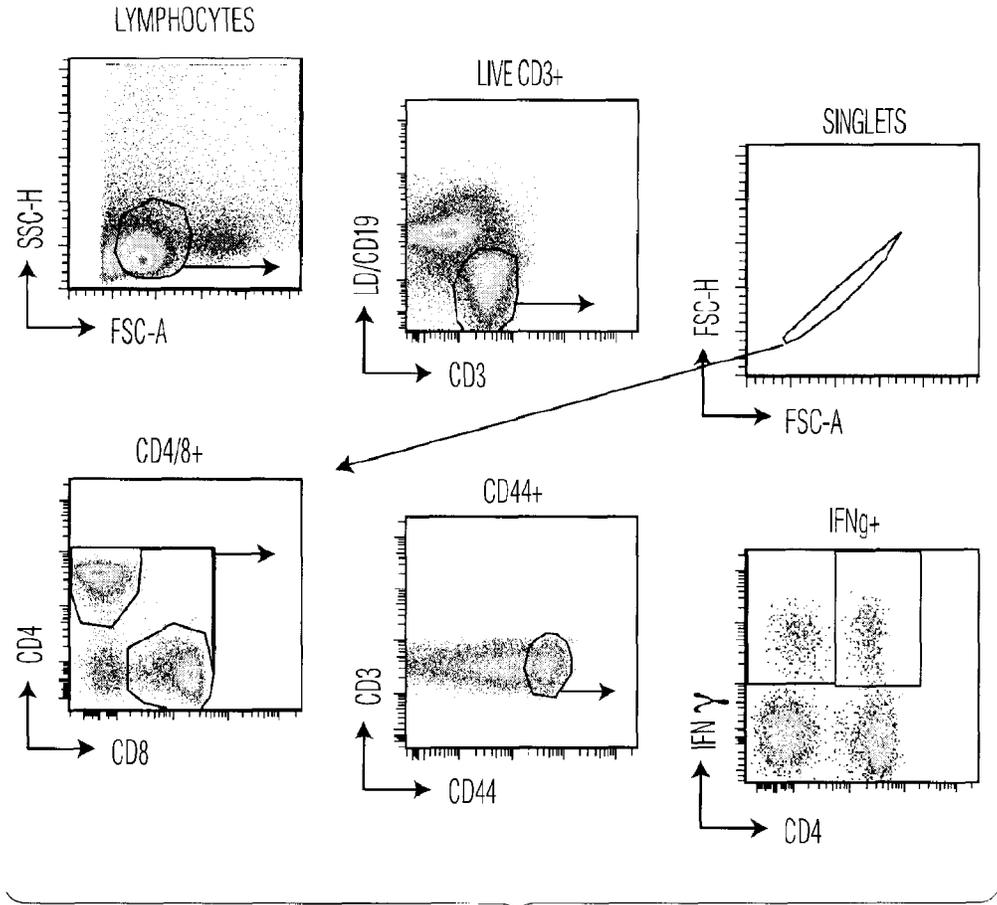


FIG. 18b

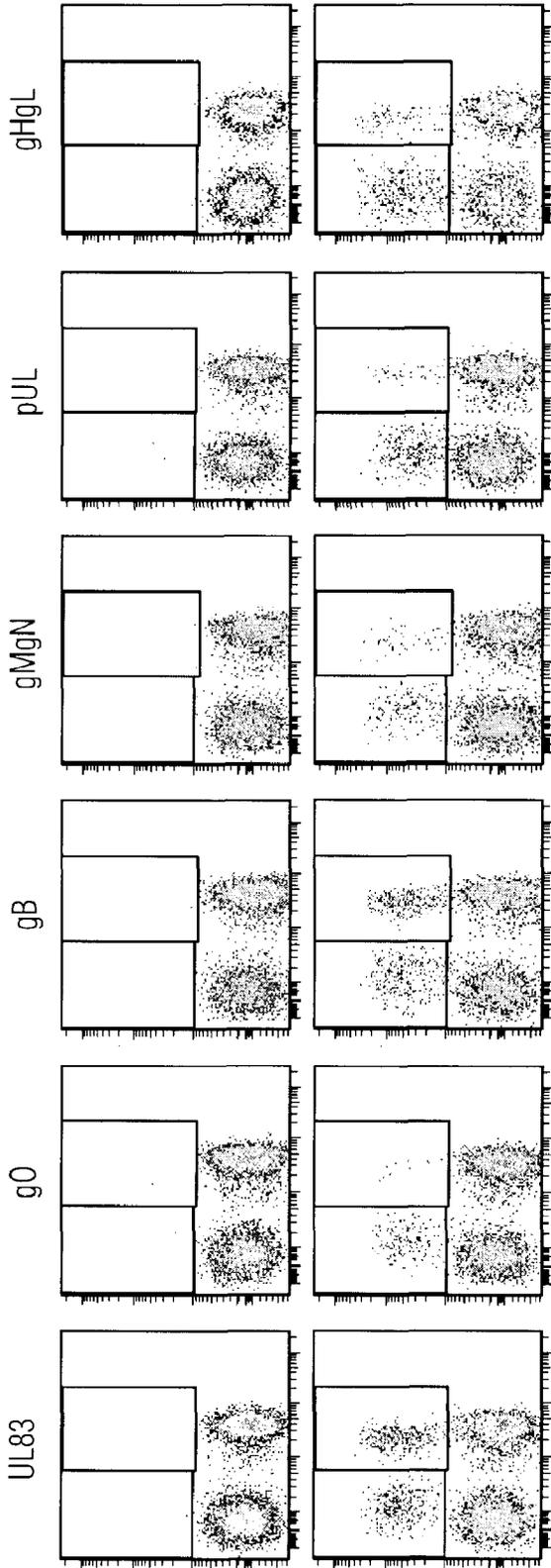


FIG. 18c

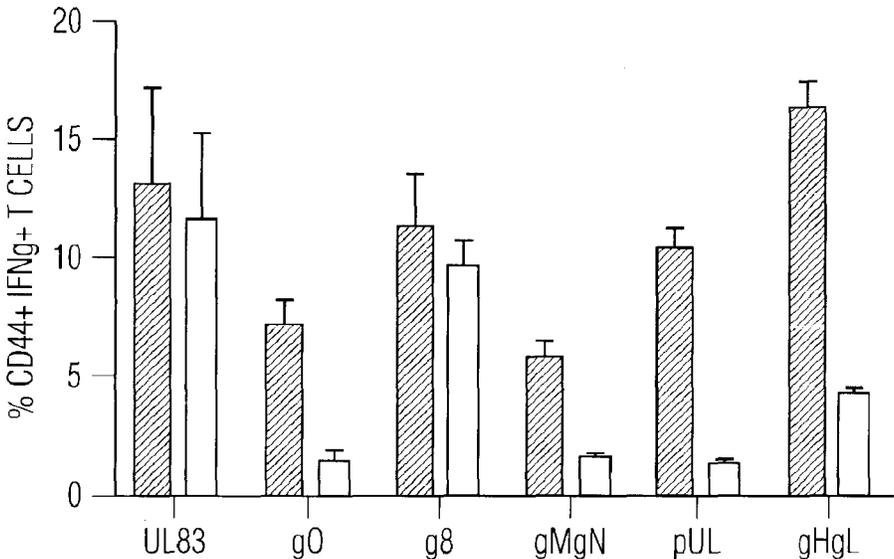


FIG. 18d

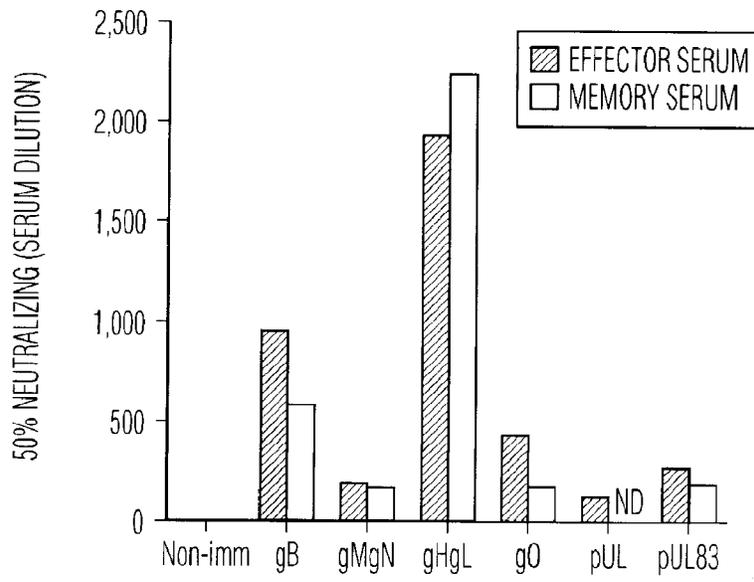


FIG. 19a

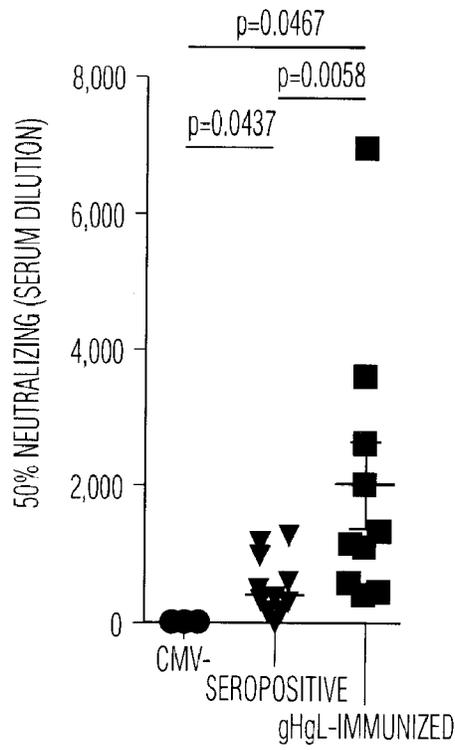


FIG. 19b

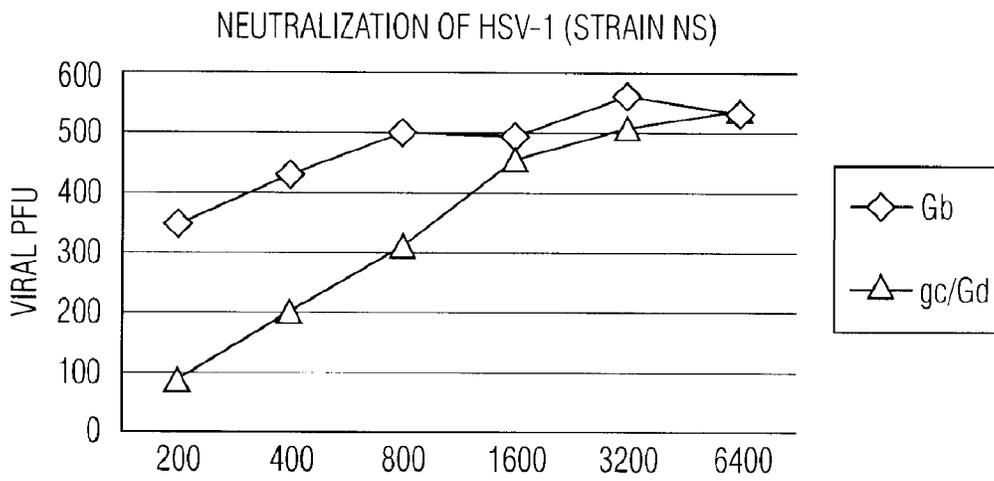


FIG. 20a

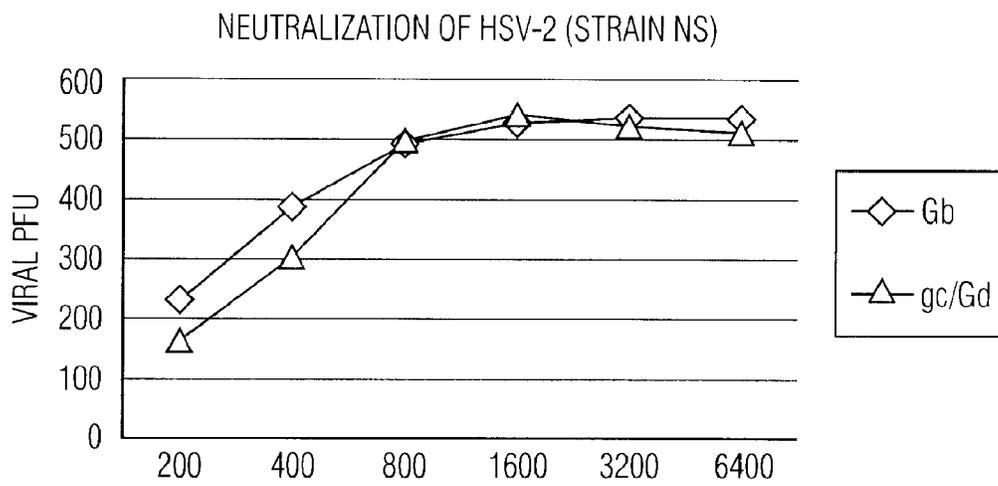


FIG. 20b

**NUCLEIC ACID MOLECULES ENCODING
NOVEL HERPES ANTIGENS, VACCINE
COMPRISING THE SAME, AND METHODS
OF USE THEREOF**

CROSS-REFERENCE TO RELATED
APPLICATIONS

This application is a divisional of U.S. patent application Ser. No. 13/982,457, filed Oct. 4, 2013, which is the U.S. national phase application filed under 35 U.S.C. § 371 claiming benefit to International Patent Application No. PCT/US12/023398, filed Jan. 31, 2012, which is entitled to priority under 35 U.S.C § 119(e) to U.S. Provisional Patent Application No. 61/438,089, filed Jan. 31, 2011, each of which applications are incorporated by reference herein in their entireties.

FIELD OF THE INVENTION

The present invention relates to nucleic acid sequences encoding human herpes family viral (Herp) proteins and fragments thereof; to improved herpes vaccines, improved methods for inducing immune responses against herpes, improved methods for prophylactically and/or therapeutically immunizing individuals against herpes viruses.

BACKGROUND OF THE INVENTION

Herpesviridae (herpesviruses or herpes family viruses) is the name of a family of enveloped, double-stranded DNA viruses with relatively large complex genomes. They replicate in the nucleus of a wide range of vertebrate hosts, including eight varieties isolated in humans, several each in horses, cattle, mice, pigs, chickens, turtles, lizards, fish, and even in some invertebrates, such as oysters. Human herpesvirus infections are endemic and sexual contact is a significant method of transmission for several including both herpes simplex virus 1 and 2 (HSV-1, HSV-2), also human cytomegalovirus (HHV-5) and likely Kaposi's sarcoma herpesvirus (HHV-8). The increasing prevalence of genital herpes and corresponding rise of neonatal infection and the implication of Epstein-Barr virus (HHV-4) and Kaposi's sarcoma herpesvirus as cofactors in human cancers create an urgency for a better understanding of this complex, and highly successful virus family.

The virion structure of all herpesvirus virions are comprised of four structural elements: 1. Core: The core consists of a single linear molecule of dsDNA in the form of a torus. 2. Capsid: Surrounding the core is an icosahedral capsid with a 100 nm diameter constructed of 162 capsomeres. 3. Tegument: Between the capsid and envelope is an amorphous, sometimes asymmetrical, feature named the tegument. It consists of viral enzymes, some of which are needed to take control of the cell's chemical processes and subvert them to virion production, some of which defend against the host cell's immediate responses, and others for which the function is not yet understood. 4. Envelope: The envelope is the outer layer of the virion and is composed of altered host membrane and a dozen unique viral glycoproteins. They appear in electron micrographs as short spikes embedded in the envelope.

The herpesvirus genomes range in length from 120 to 230 kbp with base composition from 31% to 75% G+C content and contain 60 to 120 genes. Because replication takes place inside the nucleus, herpesviruses can use both the host's transcription machinery and DNA repair enzymes to support

a large genome with complex arrays of genes. Herpesvirus genes, like the genes of their eukaryotic hosts, are not arranged in operons and in most cases have individual promoters. However, unlike eukaryotic genes, very few herpesvirus genes are spliced.

The genes are characterized as either essential or dispensable for growth in cell culture. Essential genes regulate transcription and are needed to construct the virion. Dispensable genes for the most part function to enhance the cellular environment for virus production, to defend the virus from the host immune system and to promote cell to cell spread. The large numbers of dispensable genes are in reality required for a productive *in vivo* infection. It is only in the restricted environment of laboratory cell cultures that they are dispensable. All herpesvirus genomes contain lengthy terminal repeats both direct and inverted. There are six terminal repeat arrangements and understanding how these repeats function in viral success is an interesting part of current research.

Four biological properties that characterize members of the herpesviridae family are that herpesviruses express a large number of enzymes involved in metabolism of nucleic acid (e.g. thymidine kinase), DNA synthesis (e.g. DNA helicase/primase) and processing of proteins (e.g. protein kinase); herpesviruses synthesize viral genomes and assemble capsids within the nucleus; their productive viral infection is accompanied by inevitable cell destruction; and herpesviruses are able to establish and maintain a latent state in their host and reactivate following cellular stress. Latency involves stable maintenance of the viral genome in the nucleus with limited expression of a small subset of viral genes.

Herpes virus family, which includes cytomegalovirus and herpes simplex virus, is found in the body fluids of infected individuals including urine, saliva, breast milk, blood, tears, semen, and vaginal fluids.

In the U.S., between 50% and 80% of adults are positive for HCMV by the age of 40 and there is no cure. While most infections are 'silent', HCMV can cause disease in unborn babies and immunocompromised people. HCMV in positive mothers can lead to Down syndrome, fetal alcohol syndrome, and neural tube defects. Furthermore, approximately 33% of women who become infected with HCMV for the first time during pregnancy pass the virus to unborn babies. Currently, 1 in 150 babies is born with congenital HCMV infection and 1 in 750 babies is born with or develops permanent disabilities due to HCMV. Moreover, HCMV is widespread in developing countries and areas of lower socioeconomic conditions. Therefore, developing a preventative and/or therapeutic vaccine against HCMV would decrease morbidity and medical costs associated with virus-associated illness and disease worldwide.

Current vaccine strategies using attenuated/killed virus or recombinant proteins have been reported to yield levels of efficacy approaching 35% at best. Since antibodies (Abs) recognizing viral glycoproteins such as gB, gH, gM, and gN are observed in cases of protection, it is thought that the elicitation of neutralizing Abs against these viral surface targets are important. Furthermore, T cell epitopes are known to occur in particular viral proteins including UL83 (pp65), which specifically defines T-cell-based vaccine approaches targeting pp65 epitopes.

The direct administration of nucleic acid sequences to vaccinate against animal and human diseases has been studied and much effort has focused on effective and efficient means of nucleic acid delivery in order to yield

necessary expression of the desired antigens, resulting immunogenic response and ultimately the success of this technique.

DNA vaccines have many conceptual advantages over more traditional vaccination methods, such as live attenuated viruses and recombinant protein-based vaccines. DNA vaccines are safe, stable, easily produced, and well tolerated in humans with preclinical trials indicating little evidence of plasmid integration [Martin, T., et al., Plasmid DNA malaria vaccine: the potential for genomic integration after intramuscular injection. *Hum Gene Ther*, 1999. 10(5): p. 759-68; Nichols, W. W., et al., Potential DNA vaccine integration into host cell genome. *Ann N Y Acad Sci*, 1995. 772: p. 30-9]. In addition, DNA vaccines are well suited for repeated administration due to the fact that efficacy of the vaccine is not influenced by pre-existing antibody titers to the vector [Chattergoon, M., J. Boyer, and D. B. Weiner, Genetic immunization: a new era in vaccines and immune therapeutics. *FASEB J*, 1997. 11(10): p. 753-63]. However, one major obstacle for the clinical adoption of DNA vaccines has been a decrease in the platform's immunogenicity when moving to larger animals [Liu, M. A. and J. B. Ulmer, Human clinical trials of plasmid DNA vaccines. *Adv Genet*, 2005. 55: p. 25-40]. Recent technological advances in the engineering of DNA vaccine immunogen, such as codon optimization, RNA optimization and the addition of immunoglobulin leader sequences have improved expression and immunogenicity of DNA vaccines [Andre, S., et al., Increased immune response elicited by DNA vaccination with a synthetic gp 120 sequence with optimized codon usage. *J Virol*, 1998. 72(2): p. 1497-503; Deml, L., et al., Multiple effects of codon usage optimization on expression and immunogenicity of DNA candidate vaccines encoding the human immunodeficiency virus type 1 Gag protein. *J Virol*, 2001. 75(22): p. 10991-1001; Laddy, D. J., et al., Immunogenicity of novel consensus-based DNA vaccines against avian influenza. *Vaccine*, 2007. 25(16): p. 2984-9; Frelin, L., et al., Codon optimization and mRNA amplification effectively enhances the immunogenicity of the hepatitis C virus nonstructural 3/4A gene. *Gene Ther*, 2004. 11(6): p. 522-33], as well as, recently developed technology in plasmid delivery systems such as electroporation [Hirao, L. A., et al., Intradermal/subcutaneous immunization by electroporation improves plasmid vaccine delivery and potency in pigs and rhesus macaques. *Vaccine*, 2008. 26(3): p. 440-8; Luckay, A., et al., Effect of plasmid DNA vaccine design and in vivo electroporation on the resulting vaccine-specific immune responses in rhesus macaques. *J Virol*, 2007. 81(10): p. 5257-69; Ahlen, G., et al., In vivo electroporation enhances the immunogenicity of hepatitis C virus nonstructural 3/4A DNA by increased local DNA uptake, protein expression, inflammation, and infiltration of CD3+ T cells. *J Immunol*, 2007. 179(7): p. 4741-53]. In addition, studies have suggested that the use of consensus immunogens can be able to increase the breadth of the cellular immune response as compared to native antigens alone [Yan, J., et al., Enhanced cellular immune responses elicited by an engineered HIV-1 subtype B consensus-based envelope DNA vaccine. *Mol Ther*, 2007. 15(2): p. 411-21; Rolland, M., et al., Reconstruction and function of ancestral center-of-tree human immunodeficiency virus type 1 proteins. *J Virol*, 2007. 81(16): p. 8507-14].

One method for delivering nucleic acid sequences such as plasmid DNA is the electroporation (EP) technique. The technique has been used in human clinical trials to deliver anti-cancer drugs, such as bleomycin, and in many preclinical studies on a large number of animal species.

There remains a need for nucleic acid constructs that encode herpesvirus antigens and for compositions useful to induce immune responses against herpesviruses. There remains a need for effective vaccines against herpesviruses that are economical and effective.

SUMMARY OF THE INVENTION

In one aspect of the invention, there are nucleic acid molecules comprising a coding sequence for a herpes virus antigen encoding one or more proteins selected from the group consisting of: proteins comprising SEQ ID NO:2; proteins that is 95% homologous to SEQ ID NO:2; proteins comprising SEQ ID NO:4; proteins that are 95% homologous to SEQ ID NO:4; proteins comprising SEQ ID NO:6; proteins that are 95% homologous to SEQ ID NO:6; proteins comprising SEQ ID NO:8; proteins that are 95% homologous to SEQ ID NO:8; proteins comprising SEQ ID NO:10; proteins that are 95% homologous to SEQ ID NO:10; proteins comprising SEQ ID NO:12; proteins that are 95% homologous to SEQ ID NO:12; proteins comprising SEQ ID NO:14; proteins that are 95% homologous to SEQ ID NO:14; proteins comprising SEQ ID NO:16; proteins that are 95% homologous to SEQ ID NO:16; proteins comprising SEQ ID NO:18; proteins that are 95% homologous to SEQ ID NO:18; proteins comprising proteins comprising SEQ ID NO:20; proteins that are 95% homologous to SEQ ID NO:20; proteins comprising SEQ ID NO:85; proteins that are 95% homologous to SEQ ID NO:85; proteins comprising HSV1-gH (N-terminal region up to position 838 of SEQ ID NO:87), proteins that are 95% homologous to HSV1-gH; proteins comprising HSV1-gL (C-terminal region from position 846 of SEQ ID NO:87), proteins that are 95% homologous to HSV1-gL; proteins comprising HSV1-gC (N-terminal region up to position 511 of SEQ TD NO:89), proteins that are 95% homologous to HSV1-gC; proteins comprising HSV1-gD (C-terminal region from position 519 of SEQ ID NO:89), proteins that are 95% homologous to HSV1-gD; proteins comprising SEQ ID NO:91; proteins that are 95% homologous to SEQ ID NO:91; proteins comprising HSV2-gH (N-terminal region up to position 838 of SEQ ID NO:93), proteins that are 95% homologous to HSV2-gH; proteins comprising HSV2-gL (C-terminal region from position 846 of SEQ ID NO:93), proteins that are 95% homologous to HSV2-gL; proteins comprising HSV2-gC (N-terminal region up to position 480 of SEQ ID NO:95), proteins that are 95% homologous to HSV2-gC; proteins comprising HSV2-gD (C-terminal region from position 488 of SEQ ID NO:95), proteins that are 95% homologous to HSV2-gD; proteins comprising SEQ ID NO:97; proteins that are 95% homologous to SEQ ID NO:97; proteins comprising VZV-gH (N-terminal region up to position 841 of SEQ TD NO:99), proteins that are 95% homologous to VZV-gH; proteins comprising VZV-gL (C-terminal region from position 849 of SEQ ID NO:99), proteins that are 95% homologous to VZV-gL; proteins comprising VZV-gM (N-terminal region up to position 435 of SEQ ID NO:101), proteins that are 95% homologous to VZV-gM; proteins comprising VZV-gN (C-terminal region from position 443 of SEQ ID NO:101), proteins that are 95% homologous to VZV-gN; proteins comprising SEQ ID NO:103; proteins that are 95% homologous to SEQ ID NO:103; proteins comprising CeHV1-gH (N-terminal region up to position 858 of SEQ ID NO:105), proteins that are 95% homologous to CeHV1-gH; proteins comprising CeHV1-gL (C-terminal region from position 866 of SEQ ID NO:105), proteins that are 95% homologous to CeHV1-gL;

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proteins comprising CeHV1-gC (N-terminal region up to position 467 of SEQ ID NO:107), proteins that are 95% homologous to CeHV1-gC; proteins comprising CeHV1-gD (C-terminal region from position 475 of SEQ ID NO:107), proteins that are 95% homologous to CeHV1-gD; proteins comprising VZV-gE (N-terminal region up to position 623 of SEQ ID NO:109), proteins that are 95% homologous to VZV-gE; proteins comprising VZV-gI (C-terminal region from position 631 of SEQ ID NO:109), proteins that are 95% homologous to VZV-gI; proteins comprising SEQ ID NO:111, proteins that are 95% homologous to SEQ ID NO:111; and proteins comprising SEQ ID NO:113, proteins that are 95% homologous to SEQ ID NO:113; and immunogenic fragments thereof comprising at least 10 amino acids.

In some examples, proteins set forth above comprise a signal peptide, such as for example the IgE signal peptide (SEQ ID NO: 61) (e.g. SEQ ID NOs: 22, 24, 26, 28, 30, 32, 34, 36, 38 and 40) and/or an antigenic tag such as the HA Tag (SEQ ID NO: 62) (e.g. SEQ ID NOs: 42, 44, 46, 48, 50, 52, 54, 56, 58 and 60). Further, one or more proteins set forth above may be linked to each other to form a fusion protein. In some examples, the proteins are linked by way of a proteolytic cleavage site such as the furin site (SEQ ID NO: 63) (e.g. SEQ ID NOs:65, 67, 69, 71, 73, 75, 87, 89, 93, 95, 99, 101, 105, and 107).

Nucleic acid molecules comprising sequences that encode one or more protein molecules set forth above are also provided. In some embodiments, the nucleic acid molecule comprises a sequence selected from the group consisting of: nucleic acid sequences comprising SEQ ID NO:1; nucleic acid sequences that are 95% homologous to SEQ ID NO:1; nucleic acid sequences comprising SEQ ID NO:3; nucleic acid sequences that are 95% homologous to SEQ TD NO:3; nucleic acid sequences comprising SEQ TD NO:5; nucleic acid sequences that are 95% homologous to SEQ ID NO:5; nucleic acid sequences comprising SEQ ID NO:7; nucleic acid sequences that are 95% homologous to SEQ ID NO:7; nucleic acid sequences comprising SEQ ID NO:9; nucleic acid sequences that are 95% homologous to SEQ ID NO:9; nucleic acid sequences comprising SEQ ID NO:11; nucleic acid sequences that are 95% homologous to SEQ ID NO:11; nucleic acid sequences comprising SEQ ID NO:13; nucleic acid sequences that are 95% homologous to SEQ ID NO:13; nucleic acid sequences comprising SEQ ID NO:15; nucleic acid sequences that are 95% homologous to SEQ ID NO:15; nucleic acid sequences comprising SEQ ID NO:17; nucleic acid sequences that are 95% homologous to SEQ ID NO:17; nucleic acid sequences comprising SEQ ID NO:19; nucleic acid sequences that are 95% homologous to SEQ ID NO:19; nucleic acid sequences comprising SEQ ID NO:86; nucleic acid sequences that are 95% homologous to SEQ ID NO:86; nucleic acid sequences comprising DNA sequence encoding HSV1-gH; nucleic acid sequences that are 95% homologous to DNA sequence encoding HSV1-gH; nucleic acid sequences comprising DNA sequence encoding HSV1-gL; nucleic acid sequences that are 95% homologous to DNA sequence encoding HSV1-gL; nucleic acid sequences comprising DNA sequence encoding HSV1-gC; nucleic acid sequences that are 95% homologous to DNA sequence encoding HSV1-gC; nucleic acid sequences comprising DNA sequence encoding HSV1-gD; nucleic acid sequences that are 95% homologous to DNA sequence encoding HSV1-gD; nucleic acid sequences comprising SEQ ID NO:92; nucleic acid sequences that are 95% homologous to SEQ ID NO:92; nucleic acid sequences comprising DNA sequence encoding HSV2-gH; nucleic acid sequences that

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are 95% homologous to DNA sequence encoding HSV2-gH; nucleic acid sequences comprising DNA sequence encoding HSV2-gL; nucleic acid sequences that are 95% homologous to DNA sequence encoding HSV2-gL; nucleic acid sequences comprising DNA sequence encoding HSV2-gC; nucleic acid sequences that are 95% homologous to DNA sequence encoding HSV2-gC; nucleic acid sequences comprising DNA sequence encoding HSV2-gD; nucleic acid sequences that are 95% homologous to DNA sequence encoding HSV2-gD; nucleic acid sequences comprising SEQ ID NO:98; nucleic acid sequences that are 95% homologous to SEQ ID NO:98; nucleic acid sequences comprising DNA sequence encoding VZV-gH; nucleic acid sequences that are 95% homologous to DNA sequence encoding VZV-gH; nucleic acid sequences comprising DNA sequence encoding VZV-gL; nucleic acid sequences that are 95% homologous to DNA sequence encoding VZV-gL; nucleic acid sequences comprising DNA sequence encoding VZV-gM; nucleic acid sequences that are 95% homologous to DNA sequence encoding VZV-gM; nucleic acid sequences comprising DNA sequence encoding VZV-gN; nucleic acid sequences that are 95% homologous to DNA sequence encoding VZV-gN; nucleic acid sequences comprising SEQ ID NO:104; nucleic acid sequences that are 95% homologous to SEQ ID NO:104; nucleic acid sequences comprising DNA sequence encoding CeHV1-gH; nucleic acid sequences that are 95% homologous to DNA sequence encoding CeHV1-gH; nucleic acid sequences comprising DNA sequence encoding CeHV1-gL; nucleic acid sequences that are 95% homologous to DNA sequence encoding CeHV1-gL; nucleic acid sequences comprising DNA sequence encoding CeHV1-gC; nucleic acid sequences that are 95% homologous to DNA sequence encoding CeHV1-gC; nucleic acid sequences comprising DNA sequence encoding CeHV1-gD; nucleic acid sequences that are 95% homologous to DNA sequence encoding CeHV1-gD; nucleic acid sequences comprising DNA sequence encoding VZV-gE; nucleic acid sequences that are 95% homologous to DNA sequence encoding VZV-gE; nucleic acid sequences comprising DNA sequence encoding VZV-gI; nucleic acid sequences that are 95% homologous to DNA sequence encoding VZV-gI; nucleic acid sequences comprising SEQ ID NO:112; nucleic acid sequences that are 95% homologous to SEQ ID NO:112; and nucleic acid sequences comprising SEQ ID NO:114; nucleic acid sequences that are 95% homologous to SEQ ID NO:114; and fragments thereof that comprise nucleic acid sequences encoding immunogenic fragments comprising at least 10 amino acids.

In some examples, the nucleic acid sequences encode proteins that further comprise a signal peptide, such as for example the IgE signal peptide (DNA sequence encoding SEQ ID NO: 61) (e.g. SEQ ID NOs: 21, 23, 25, 27, 29, 31, 33, 35, 37 and 39) and/or an antigenic tag such as the HA Tag (DNA sequence encoding SEQ ID NO:62) (e.g. SEQ ID NOs: 41, 43, 45, 47, 49, 51, 53, 55, 57 and 59). Further, one or more nucleic acid sequences may be linked to each other to form a chimeric gene that encodes a fusion protein. In some examples, the nucleic acid sequences encode proteins that are linked by way of a proteolytic cleavage site such as the furin site (DNA sequence encoding SEQ ID NO:63) (e.g. SEQ ID NOs:64, 66, 68, 70, 72, 74, 88, 90, 94, 96, 100, 102, 106, 108, and 110).

In some embodiments, the nucleic acid molecules comprising sequences that encode one or more protein molecules set forth above are also provided in combination with a different second nucleic acid sequence, wherein the second

nucleic acid sequence encodes a protein selected from the group consisting of: HCMV gB, HCMV gM, HCMV gN, HCMV gH, HCMV gL, HCMV gO, HCMV-UL131a, HCMV-UL130, HCMV-UL128, HCMV-UL83, HSV1-gB, HSV1-gH, HSV1-gL, HSV1-gC, HSV1-gD, HSV2-gB, HSV2-gH, HSV2-gL, HSV2-gC, HSV2-gD, VZV-gB, VZV-gH, VZV-gL, VZV-gM, VZV-gN, VZV-gE, VZV-gI, VZV-gC, VZV-gK, CeHV1-gB, CeHV1-gH, CeHV1-gL, CeHV1-gC, and CeHV1-gD. Preferably, an HCMV sequence will be combined with a different second HCMV sequence; an HSV1 sequence will be combined with a different second HSV1 sequence; an HSV2 sequence will be combined with a different second HSV2 sequence; an CeHV1 sequence will be combined with a different second CeHV1 sequence; and a VZV sequence will be combined with a different second VZV sequence.

Another aspect of the present invention includes compositions that comprise one or more of the nucleic acid molecules provided herein.

Some aspects of the invention provide method of inducing an immune response against a herpes virus antigen comprising administering the nucleic acid molecules provided herein. Preferably the herpes virus antigens comprise HCMV, HSV1, HSV2, CeHV1, and VZV antigens.

Additional aspects of the invention provide methods of protecting an individual from herpes virus infection comprising administering the nucleic acid molecules provided herein. In some embodiments, the individual is an individual who has been diagnosed with herpes virus infection.

In another aspect of the invention, there are proteins selected from the group consisting of: a protein comprising SEQ ID NO:2; a protein that is 95% homologous to SEQ ID NO:2; a protein comprising SEQ ID NO:4; a protein that is 95% homologous to SEQ ID NO:4; a protein comprising SEQ ID NO:6; a protein that is 95% homologous to SEQ ID NO:6; a protein comprising SEQ ID NO:8; a protein that is 95% homologous to SEQ ID NO:8; a protein comprising SEQ ID NO:10; a protein that is 95% homologous to SEQ ID NO:10; a protein comprising SEQ ID NO:12; a protein that is 95% homologous to SEQ ID NO:12; a protein comprising SEQ ID NO:14; a protein that is 95% homologous to SEQ ID NO:14; a protein comprising SEQ TD NO:16; a protein that is 95% homologous to SEQ TD NO:16; a protein comprising SEQ ID NO:18; a protein that is 95% homologous to SEQ ID NO:18; a protein comprising a protein comprising SEQ ID NO:20; a protein that is 95% homologous to SEQ ID NO:20; a protein comprising SEQ ID NO:85, proteins that are 95% homologous to SEQ ID NO:85; a protein comprising HSV1-gH (N-terminal region up to position 838 of SEQ ID NO:87), proteins that are 95% homologous to HSV1-gH; a protein comprising HSV1-gL (C-terminal region from position 846 of SEQ ID NO:87), proteins that are 95% homologous to HSV1-gL; a protein comprising HSV1-gC (N-terminal region up to position 511 of SEQ ID NO:89), proteins that are 95% homologous to HSV1-gC; a protein comprising HSV1-gD (C-terminal region from position 519 of SEQ ID NO:89), proteins that are 95% homologous to HSV1-gD; a protein comprising SEQ ID NO:91, proteins that are 95% homologous to SEQ ID NO:91; a protein comprising HSV2-gH (N-terminal region up to position 838 of SEQ ID NO:93), proteins that are 95% homologous to HSV2-gH; a protein comprising HSV2-gL (C-terminal region from position 846 of SEQ ID NO:93), proteins that are 95% homologous to HSV2-gL; a protein comprising HSV2-gC (N-terminal region up to position 480 of SEQ ID NO:95), proteins that are 95% homologous to HSV2-gC; a protein comprising HSV2-gD (C-ter-

terminal region from position 488 of SEQ ID NO:95), proteins that are 95% homologous to HSV2-gD; a protein comprising SEQ ID NO:97, proteins that are 95% homologous to SEQ ID NO:97; a protein comprising VZV-gH (N-terminal region up to position 841 of SEQ ID NO:99), proteins that are 95% homologous to VZV-gH; a protein comprising VZV-gL (C-terminal region from position 849 of SEQ ID NO:99), proteins that are 95% homologous to VZV-gL; a protein comprising VZV-gM (N-terminal region up to position 435 of SEQ ID NO:101), proteins that are 95% homologous to VZV-gM; a protein comprising VZV-gN (C-terminal region from position 443 of SEQ ID NO:101), proteins that are 95% homologous to VZV-gN; a protein comprising SEQ ID NO:103, proteins that are 95% homologous to SEQ ID NO:103; a protein comprising CeHV1-gH (N-terminal region up to position 858 of SEQ ID NO:105), proteins that are 95% homologous to CeHV1-gH; a protein comprising CeHV1-gL (C-terminal region from position 866 of SEQ ID NO:105), proteins that are 95% homologous to CeHV1-gL; a protein comprising CeHV1-gC (N-terminal region up to position 467 of SEQ ID NO:107), proteins that are 95% homologous to CeHV1-gC; a protein comprising CeHV1-gD (C-terminal region from position 475 of SEQ TD NO:107), proteins that are 95% homologous to CeHV1-gD; a protein comprising VZV-gE (N-terminal region up to position 623 of SEQ ID NO:109), proteins that are 95% homologous to VZV-gE; a protein comprising VZV-gI (C-terminal region from position 631 of SEQ ID NO:109), proteins that are 95% homologous to VZV-gI; a protein comprising SEQ ID NO:111, proteins that are 95% homologous to SEQ ID NO:111; and a protein comprising SEQ ID NO:113, proteins that are 95% homologous to SEQ ID NO:113; and immunogenic fragments thereof comprising at least 10 amino acids.

In some embodiments, there are provided methods of inducing an immune response against a herpes virus infection comprising delivering to an individual the proteins provided herein. In some embodiments, the individual is an individual who has been diagnosed with herpes virus infection.

Aspects of the invention relate to method of generating a multivalent vaccine against a herpes family virus, comprising: performing phylogenetic and molecular evolutionary analysis to estimate diversity among clinically relevant and publically available target protein sequences of the herpes virus; selecting at least two target protein sequence from the group comprising: a) a specific, clinically relevant subgroup of a divergent protein; or b) a highly conserved protein; generating a consensus sequence from the selected target protein sequences; and cloning the consensus target protein sequences from the generating step into one or more expression constructs for formulation of the multivalent vaccine. In some embodiments, the the selecting step comprises selecting target proteins that are associated to one another as part of a biological complex expressed by a herpes virus. In some embodiments, the selected target proteins are surface antigens. In some embodiments the surface antigens are selected from the group consisting of gH, gL, gM, gN, gC, and gD. In some embodiments, the surface antigens are gH and gL. In some embodiments, the specific, clinically relevant subgroup of a divergent protein further comprises, selecting a clinically relevant strain of the herpes virus that has passaged no more than four times in culture. In some embodiments, the step of selecting the specific, clinically relevant subgroup of a divergent protein further comprises, selecting a clinically relevant strain of the herpes virus that has passaged no more than six times in culture. In some embodi-

ments, the herpes family virus is selected from the group consisting of CMV, HSV1, HSV2, VZV, CeHV1, EBV, roseolovirus, Kaposi's sarcoma-associated herpesvirus, and MuHV.

Another aspect of the invention comprises methods of generating a multivalent vaccine against a herpes family virus, comprising: performing phylogenetic and molecular evolutionary analysis to estimate diversity among clinically relevant and publically available target protein sequences of the herpes virus; selecting at least two target protein sequence from the group comprising: a) a specific, clinically relevant subgroup of a divergent protein; or b) a highly conserved protein; generating a consensus sequence from the selected target protein sequences; and cloning the consensus target protein sequences from the generating step into one or more expression constructs for formulation of the multivalent vaccine. The expression constructs can be formulated with known and available pharmaceutically acceptable excipients. In some embodiments, the multivalent vaccines can also include a known vaccine adjuvant, preferably IL-12, IL-15, IL-28, and RANTES.

In some embodiments the herpes family virus is selected from CMV, HSV1, HSV2, VZV, CeHV1, EBV, roseolovirus, Kaposi's sarcoma-associated herpesvirus, or MuHV, and preferably, CMV, HSV1, HSV2, CeHV1 or VZV.

In some embodiments, the selected target proteins are those associated to one another as part of a biological complex expressed by a herpes virus. Preferably, the selected target proteins are surface antigens, more preferably antigens gH, gL, gM, gN, gC, and gD, and even more preferably the surface antigens are gH and gL.

In some embodiments, the step of selecting the specific, clinically relevant subgroup of a divergent protein further comprises, selecting a clinically relevant strain of the herpes virus that has passed no more than four times in culture, and preferably no more than six times.

Aspects of the invention relates to vaccines against viruses of the herpes families which comprise coding sequence for two or more antigens. In some embodiments, two or more such antigens are provided on the same vector such as a plasmid to ensure co-expression of both antigens in the same cell. Various permutations of antigens are provided as are various arrangements in which multiple plasmids are provided encoding such multiple antigens including embodiments in which two or more such antigens are provided on the same vector. For example, co-expression of the the combination of gH and gL antigens from HCMV and HSV1 have both been observed to provide antigen transport to the cell surface which does not occur when proteins are expressed in the absence of each other. Data show the coexpression of gH and gL provide more effective immune targets than when proteins are expressed in the absence of each other. According to aspects of the invention, multiple antigens may be delivered as coding sequences to provide effective vaccines. In some embodiments, coding sequences for multiple antigens are provided on single vectors such as single plasmids.

BRIEF DESCRIPTION OF THE FIGURES

FIG. 1 is a map of the pVax1 variant used as a backbone for plasmids with herpes virus coding sequence inserts. The sequence of the pVax1 Variant is set forth in SEQ ID NO:76.

FIG. 2 is a plasmid map of plasmid 1 described in Example 1. Plasmid 1 is also referred to as pHCMVgB or pHCMVgB_pVAX1. The sequence of pHCMVgB_pVAX1 is set forth in SEQ ID NO:77.

FIG. 3 is a plasmid map of plasmid 2 described in Example 1. Plasmid 2 is also referred to as pHCMVgMgN or pHCMVgMgN_pVAX1. The sequence of pHCMVgMgN_pVAX1 is set forth in SEQ ID NO:78.

FIG. 4 is a plasmid map of plasmid 3 described in Example 1. Plasmid 3 is also referred to as pHCMVgHgL or pHCMVgHgL_pVAX1. The sequence of pHCMVgHgL_pVAX1 is set forth in SEQ ID NO:79.

FIG. 5 is a plasmid map of plasmid 4 described in Example 1. Plasmid 4 is also referred to as pHCMVgO or pHCMVgO_pVAX1. The sequence of pHCMVgO_pVAX1 is set forth in SEQ ID NO:80.

FIG. 6 is a plasmid map of plasmid 5 described in Example 1. Plasmid 5 is also referred to as pHCMVgUL or pHCMVgUL_pVAX1. The sequence of pHCMVgUL_pVAX1 is set forth in SEQ ID NO:81.

FIG. 7 is a plasmid map of modified plasmid 1 described in Example 1. Modified plasmid 1 is different from plasmid 1 in that modified plasmid 1 does not contain coding sequences for HA Tags linked to the coding sequences for HCMV gB antigen sequence. Modified plasmid 1 is also referred to as pHCMVgB or pHCMV_gB_pVAX1. The sequence of pHCMV_gB_pVAX1 is set forth in SEQ ID NO:82.

FIG. 8 is a plasmid map of modified plasmid 3 described in Example 1. Modified plasmid 3 is different from plasmid 3 in that modified plasmid 3 does not contain coding sequences for HA Tags linked to the coding sequences for HCMV gH and gL antigen sequences. Modified plasmid 3 is also referred to as pHCMVgHgL or pHCMV_gHgL_pVAX1. The sequence of pHCMV_gHgL_pVAX1 is set forth in SEQ ID NO:83.

FIG. 9 is a plasmid map of modified plasmid 6 described in Example 1. Modified plasmid 6 is different from plasmid 6 (not shown) in that modified plasmid 6 does not contain coding sequences for HA Tags linked to the coding sequences for HCMV gU83 antigen sequence. Modified plasmid 6 is also referred to as pHCMVgU83 or pHCMV_UL83_pVAX1. The sequence of pHCMV_UL83_pVAX1 is set forth in SEQ ID NO:84.

FIG. 10 shows data from experiments identifying immunodominant epitopes of HCMV-gB using plasmid 1.

FIG. 11 shows data from experiments identifying immunodominant epitopes of HCMV-gH and HCMV-gL using plasmid 3.

FIG. 12 shows data from experiments identifying immunodominant epitopes of HCMV-gM and HCMV-gN using plasmid 2 and of HCMV-gO using plasmid 4.

FIG. 13 shows data from experiments identifying immunodominant epitopes of HCMV-UL83 using modified plasmid 6 and HCMV-UL131A, HCMV-UL130, and HCMV-UL128 using plasmid 5.

FIG. 14 shows neutralizing antibody titers of mouse serum from mice immunized with HCMV proteins. The data is expressed as a geometric mean of 3 values with 95% CI. Life-extended HFF (human foreskin fibroblasts) cells were used.

FIG. 15 shows a summary of DNA vaccine data.

FIG. 16a-e shows graphs that show (a) two groups of mice were immunized twice with 35 μ g of pHCMV-NP in which the genetic sequences differed, derived from the virus (Native) or optimized for expression in mice (Optimized), but the encoded amino acids were identical. Splenocytes were harvested 8 days after the second immunization and NP-specific T cells were assessed by ELISPOT. (b) Mice were immunized twice with pHCMV-NP, either with or without EP, pVAX with EP (n=10), or with 2×10^5 PFU

HCMV i.p. (n=5). Mice were challenged with 20LD₅₀ HCMV i.c. 8 weeks after the second immunization or HCMV acute infection and survival data are shown. (c) Mice were immunized one, two, three or four times with or without EP, pVAX four times with EP, or HCMV acute infected. NP-specific IgG responses were evaluated 7 days following each immunization, or 60 days post-HCMV infection, and data are shown. (d) Mice were immunized twice with either 35 µg pHCMV-NP with EP or 45 µg of pHCMV-GP with EP, and viral protein-specific T cell immunity was assessed 8 days later. (e) Mice were given a single injection of 35 µg of pHCMV-NP with EP or 45 µg of pHCMV-GP with EP, pVAX with EP (n=10), or with 2×10⁵ PFU HCMV i.p. (n=5) and were later challenged with 20LD₅₀ HCMV i.c. 8 weeks after the vaccination or infection. Survival data for each group of mice are shown.

FIG. 17a-j shows schematic of phylogenetic trees of HCMV putative vaccine protein immunogens from publicly available sources are shown. Amino acid sequences were multiple-aligned with ClustalW and cluster analysis was performed by maximum-likelihood method. The significance of the unrooted phylogenetic trees was verified by bootstrap analysis and significant support values (≥80%; 1,000 bootstrap replicates) are indicated by asterisks at major nodes. Major reported genotypes are illustrated, percentages are amino acid identity positions of all full-length sequences, and reference strains are indicated; AD—AD169, DV—Davis, JH—JHC, JP—JP, ML—Merlin, TO—Toledo, TN—Towne, VR—VR 1814. DNA vaccine-encoded HCMV immunogens are also shown (Vac). Scale bars signify distance of amino acids per site and analyses were conducted using MEGA version 5.

FIG. 18a-d shows graphs and images that depict nascent co-expression of structurally-relevant HCMV immunogens induces robust immunity, including a) a graph of HCMV: gB, gM, gN, gH, gL, gO, UL128, UL130, UL131A, and UL83 domains showing immuniticity (see also FIGS. 10-13 for different graphical display of same data); b) images showing character of immune response; c) images for HCMV: UL83, gO, gB, gMgN, UL, and gHgL, and d) percent CD44+ IFNγ+ T cells for HCMV: UL83, gO, gB, gMgN, UL, and gHgL.

FIG. 19a-b shows graphs that neutralization data for: a) 50% neutralization levels for HCMV: gB, gMgN, gHgL, gO, UL, and UL83, and b) 50% neutralization levels for CMV only, seropositive serum, and HCMV-gHgL immunized serum.

FIG. 20a-b shows graphs that depict neutralization levels for a) neutralization against HSV-1 (strain NS) by HSV1-gB and HSV1-gCgD immunized serum; and b) neutralization against HSV-2 (strain MS) by HSV2-gB and HSV2-gCgD immunized serum.

DETAILED DESCRIPTION

1. Definitions

The terminology used herein is for the purpose of describing particular embodiments only and is not intended to be limiting. As used in the specification and the appended claims, the singular forms “a,” “an” and “the” include plural referents unless the context clearly dictates otherwise.

For recitation of numeric ranges herein, each intervening number there between with the same degree of precision is explicitly contemplated. For example, for the range of 6-9, the numbers 7 and 8 are contemplated in addition to 6 and

9, and for the range 6.0-7.0, the numbers 6.0, 6.1, 6.2, 6.3, 6.4, 6.5, 6.6, 6.7, 6.8, 6.9, and 7.0 are explicitly contemplated.

a. Adjuvant

“Adjuvant” as used herein means any molecule added to the DNA plasmid vaccines described herein to enhance the immunogenicity of the antigens encoded by the DNA plasmids and the encoding nucleic acid sequences described hereinafter.

b. Antibody

“Antibody” as used herein means an antibody of classes IgG, IgM, IgA, IgD or IgE, or fragments, fragments or derivatives thereof, including Fab, F(ab')₂, Fd, and single chain antibodies, diabodies, bispecific antibodies, bifunctional antibodies and derivatives thereof. The antibody can be an antibody isolated from the serum sample of mammal, a polyclonal antibody, affinity purified antibody, or mixtures thereof which exhibits sufficient binding specificity to a desired epitope or a sequence derived therefrom.

c. Coding Sequence

“Coding sequence” or “encoding nucleic acid” as used herein means the nucleic acids (RNA or DNA molecule) that comprise a nucleotide sequence which encodes a protein. The coding sequence can further include initiation and termination signals operably linked to regulatory elements including a promoter and polyadenylation signal capable of directing expression in the cells of an individual or mammal to whom the nucleic acid is administered.

d. Complement

“Complement” or “complementary” as used herein means a nucleic acid can mean Watson-Crick (e.g., A-T/U and C-G) or Hoogsteen base pairing between nucleotides or nucleotide analogs of nucleic acid molecules.

e. Consensus or Consensus Sequence

“Consensus” or “consensus sequence” as used herein means a polypeptide sequence based on analysis of an alignment of multiple subtypes of a particular herpes family virus, comprising HCMV, HSV1, HSV2, CeHV1, VZV, Epstein-Barr virus (EBV), roseolovirus (or herpes lymphotropic virus), Kaposi-s sarcoma-associated herpesvirus, and murine gammaherpesvirus (MuHV-4), preferably HCMV, HSV1, HSV2, CeHV1, VZV, and more preferably HCMV, HSV1, HSV2, and VZV antigen. Nucleic acid sequences that encode a consensus polypeptide sequence may be prepared. Vaccines comprising proteins that comprise consensus sequences and/or nucleic acid molecules that encode such proteins can be used to induce broad immunity against multiple subtypes or serotypes of a particular HCMV antigen.

f. Constant Current

“Constant current” as used herein means a current that is received or experienced by a tissue, or cells defining said tissue, over the duration of an electrical pulse delivered to same tissue. The electrical pulse is delivered from the electroporation devices described herein. This current remains at a constant amperage in said tissue over the life of an electrical pulse because the electroporation device provided herein has a feedback element, preferably having instantaneous feedback. The feedback element can measure the resistance of the tissue (or cells) throughout the duration of the pulse and cause the electroporation device to alter its electrical energy output (e.g., increase voltage) so current in same tissue remains constant throughout the electrical pulse (on the order of microseconds), and from pulse to pulse. In some embodiments, the feedback element comprises a controller.

g. Current Feedback or Feedback

“Current feedback” or “feedback” can be used interchangeably and means the active response of the provided electroporation devices, which comprises measuring the current in tissue between electrodes and altering the energy output delivered by the EP device accordingly in order to maintain the current at a constant level. This constant level is preset by a user prior to initiation of a pulse sequence or electrical treatment. The feedback can be accomplished by the electroporation component, e.g., controller, of the electroporation device, as the electrical circuit therein is able to continuously monitor the current in tissue between electrodes and compare that monitored current (or current within tissue) to a preset current and continuously make energy-output adjustments to maintain the monitored current at preset levels. The feedback loop can be instantaneous as it is an analog closed-loop feedback.

h. Decentralized Current

“Decentralized current” as used herein means the pattern of electrical currents delivered from the various needle electrode arrays of the electroporation devices described herein, wherein the patterns minimize, or preferably eliminate, the occurrence of electroporation related heat stress on any area of tissue being electroporated.

i. Electroporation

“Electroporation,” “electro-permeabilization,” or “electro-kinetic enhancement” (“EP”) as used interchangeably herein means the use of a transmembrane electric field pulse to induce microscopic pathways (pores) in a bio-membrane; their presence allows biomolecules such as plasmids, oligonucleotides, siRNA, drugs, ions, and water to pass from one side of the cellular membrane to the other.

j. Feedback Mechanism

“Feedback mechanism” as used herein means a process performed by either software or hardware (or firmware), which process receives and compares the impedance of the desired tissue (before, during, and/or after the delivery of pulse of energy) with a present value, preferably current, and adjusts the pulse of energy delivered to achieve the preset value. A feedback mechanism can be performed by an analog closed loop circuit.

k. Fragment

“Fragment” as used herein with respect to nucleic acid sequences means a nucleic acid sequence or a portion thereof, that encodes a polypeptide capable of eliciting an immune response in a mammal that cross reacts with a full length wild type strain herpes family virus, comprising HCMV, HSV1, HSV2, CeHV1, VZV, Epstein-Barr virus (EBV), roseolovirus (or herpes lymphotropic virus), Kaposi-s sarcoma-associated herpesvirus, and murine gammaherpesvirus (MuHV-4), preferably HCMV, HSV1, HSV2, CeHV1, VZV, and more preferably HCMV, HSV1, HSV2, and VZV antigen. The fragments can be DNA fragments selected from at least one of the various nucleotide sequences that encode protein fragments set forth below.

“Fragment” with respect to polypeptide sequences means a polypeptide capable of eliciting an immune response in a mammal that cross reacts with a full length wild type strain herpes family virus, comprising HCMV, HSV1, HSV2, CeHV1, VZV, Epstein-Barr virus (EBV), roseolovirus (or herpes lymphotropic virus), Kaposi-s sarcoma-associated herpesvirus, and murine gammaherpesvirus (MuHV-4), preferably HCMV, HSV1, HSV2, CeHV1, VZV, and more preferably HCMV, HSV1, HSV2, and VZV antigen. Fragments of consensus proteins may comprise at least 10%, at

least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90% or at least 95% of a consensus protein.

l. Genetic Construct

As used herein, the term “genetic construct” refers to the DNA or RNA molecules that comprise a nucleotide sequence which encodes a protein. The coding sequence includes initiation and termination signals operably linked to regulatory elements including a promoter and polyadenylation signal capable of directing expression in the cells of the individual to whom the nucleic acid molecule is administered. As used herein, the term “expressible form” refers to gene constructs that contain the necessary regulatory elements operable linked to a coding sequence that encodes a protein such that when present in the cell of the individual, the coding sequence will be expressed.

m. Identical

“Identical” or “identity” as used herein in the context of two or more nucleic acids or polypeptide sequences, means that the sequences have a specified percentage of residues that are the same over a specified region. The percentage can be calculated by optimally aligning the two sequences, comparing the two sequences over the specified region, determining the number of positions at which the identical residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the specified region, and multiplying the result by 100 to yield the percentage of sequence identity. In cases where the two sequences are of different lengths or the alignment produces one or more staggered ends and the specified region of comparison includes only a single sequence, the residues of single sequence are included in the denominator but not the numerator of the calculation. When comparing DNA and RNA, thymine (T) and uracil (U) can be considered equivalent. Identity can be performed manually or by using a computer sequence algorithm such as BLAST or BLAST 2.0.

n. Impedance

“Impedance” can be used when discussing the feedback mechanism and can be converted to a current value according to Ohm’s law, thus enabling comparisons with the preset current.

o. Immune Response

“Immune response” as used herein means the activation of a host’s immune system, e.g., that of a mammal, in response to the introduction of antigen such as an herpes family virus, comprising HCMV, HSV1, HSV2, CeHV1, VZV, Epstein-Barr virus (EBV), roseolovirus (or herpes lymphotropic virus), Kaposi-s sarcoma-associated herpesvirus, and murine gammaherpesvirus (MuHV-4), preferably HCMV, HSV1, HSV2, CeHV1, VZV, and more preferably HCMV, HSV1, HSV2, and VZV consensus antigens. The immune response can be in the form of a cellular or humoral response, or both.

p. Nucleic Acid

“Nucleic acid” or “oligonucleotide” or “polynucleotide” as used herein means at least two nucleotides covalently linked together. The depiction of a single strand also defines the sequence of the complementary strand. Thus, a nucleic acid also encompasses the complementary strand of a depicted single strand. Many variants of a nucleic acid can be used for the same purpose as a given nucleic acid. Thus, a nucleic acid also encompasses substantially identical nucleic acids and complements thereof. A single strand provides a probe that can hybridize to a target sequence under stringent hybridization conditions. Thus, a nucleic

acid also encompasses a probe that hybridizes under stringent hybridization conditions.

Nucleic acids can be single stranded or double stranded, or can contain portions of both double stranded and single stranded sequence. The nucleic acid can be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid can contain combinations of deoxyribo- and ribonucleotides, and combinations of bases including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine and isoguanine. Nucleic acids can be obtained by chemical synthesis methods or by recombinant methods.

q. Operably Linked

“Operably linked” as used herein means that expression of a gene is under the control of a promoter with which it is spatially connected. A promoter can be positioned 5' (upstream) or 3' (downstream) of a gene under its control. The distance between the promoter and a gene can be approximately the same as the distance between that promoter and the gene it controls in the gene from which the promoter is derived. As is known in the art, variation in this distance can be accommodated without loss of promoter function.

r. Promoter

“Promoter” as used herein means a synthetic or naturally-derived molecule which is capable of conferring, activating or enhancing expression of a nucleic acid in a cell. A promoter can comprise one or more specific transcriptional regulatory sequences to further enhance expression and/or to alter the spatial expression and/or temporal expression of same. A promoter can also comprise distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A promoter can be derived from sources including viral, bacterial, fungal, plants, insects, and animals. A promoter can regulate the expression of a gene component constitutively, or differentially with respect to cell, the tissue or organ in which expression occurs or, with respect to the developmental stage at which expression occurs, or in response to external stimuli such as physiological stresses, pathogens, metal ions, or inducing agents. Representative examples of promoters include the bacteriophage T7 promoter, bacteriophage T3 promoter, SP6 promoter, lac operator-promoter, tac promoter, SV40 late promoter, SV40 early promoter, RSV-LTR promoter, CMV IE promoter, SV40 early promoter or SV40 late promoter and the CMV 1E promoter.

s. Signal Peptide

“Signal peptide and leader sequence” are used interchangeably herein and refer to an amino acid sequence at the amino terminus of an herpes family virus, comprising HCMV, HSV1, HSV2, CeHV1, VZV, Epstein-Barr virus (EBV), roseolovirus (or herpes lymphotropic virus), Kaposi-s sarcoma-associated herpesvirus, and murine gammaherpesvirus (MuHV-4), preferably HCMV, HSV1, HSV2, CeHV1, VZV, and more preferably HCMV, HSV1, HSV2, and VZV protein. Signal peptides/leader sequences typically direct localization of a protein. Signal peptides/leader sequences used herein preferably facilitate secretion of a protein from the cell in which it is produced. Signal peptides/leader sequences are often cleaved from the remainder of the protein, often referred to as the mature protein, upon secretion from the cell. Signal peptides/leader sequences are linked at the N terminus of the protein. As referred to herein with regard to linking a signal peptide or leader sequence to the N terminus of a protein, the signal peptide/leader sequence replaces the N terminal methionine of a protein. Thus for example, SEQ ID NO:22 is SEQ ID NO:2 with the signal peptide/leader sequence linked at the

N terminal of SEQ ID NO:2. The N terminal residue of SEQ ID NO:2 can be anything but if it is encoded by an initiation sequence it is methionine. the linkage of the signal peptide/leader sequence at the N terminal of SEQ ID NO:2 eliminates an N terminal methionine. As used herein, it is intended that SEQ ID NO:22 comprises SEQ ID NO:2 with a signal peptide/leader sequence linked at the N terminal of SEQ ID NO:2 notwithstanding the elimination of the N terminus Xaa residue of SEQ ID NO:2. Similarly, the coding sequences for SEQ ID NO:22 comprise coding sequences for SEQ ID NO:2 with coding sequences for a signal peptide/leader sequence linked to the 5' end of the coding sequences encoding SEQ ID NO:2. The initiation codon may be the nnn in the coding sequences for SEQ ID NO:2 but it is eliminated when the coding sequences for a signal peptide/leader sequence linked to the 5' end of the coding sequences encoding SEQ ID NO:2. As used herein, it is intended that coding sequences for SEQ ID NO:22 comprises coding sequences for SEQ ID NO:2 with coding sequences for a signal peptide/leader sequence linked at the 5' end of the coding sequence of SEQ ID NO:2 where nnn occurs. Thus, for example, it is intended that SEQ ID NO:21 comprises SEQ ID NO:1 with coding sequences for a signal peptide/leader sequence linked at the 5' end of SEQ ID NO:1, in place of the nnn. In some embodiments, the nnn is an initiation codon at the 5' end of SEQ ID NO:1. It is further intended that SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18 and 20 are provided free of then terminal Xaa and that SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17 and 19 are provided free the nnn.

t. Stringent Hybridization Conditions

“Stringent hybridization conditions” as used herein means conditions under which a first nucleic acid sequence (e.g., probe) will hybridize to a second nucleic acid sequence (e.g., target), such as in a complex mixture of nucleic acids. Stringent conditions are sequence-dependent and will be different in different circumstances. Stringent conditions can be selected to be about 5-10° C. lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m can be the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions can be those in which the salt concentration is less than about 1.0 M sodium ion, such as about 0.01-1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C. for short probes (e.g., about 10-50 nucleotides) and at least about 60° C. for long probes (e.g., greater than about 50 nucleotides). Stringent conditions can also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal can be at least 2 to 10 times background hybridization. Exemplary stringent hybridization conditions include the following: 50% formamide, 5×SSC, and 1% SDS, incubating at 42° C., or, 5×SSC, 1% SDS, incubating at 65° C., with wash in 0.2×SSC, and 0.1% SDS at 65° C.

u. Substantially Complementary

“Substantially complementary” as used herein means that a first sequence is at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98% or 99% identical to the complement of a second sequence over a region of 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 180, 270, 360, 450, 540, 630, 720, 810, 900, 990, 1080, 1170, 1260, 1350, 1440, 1530, 1620, 1710, 1800, 1890, 1980, 2070 or more

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nucleotides or amino acids, or that the two sequences hybridize under stringent hybridization conditions.

v. Substantially Identical

“Substantially identical” as used herein means that a first and second sequence are at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98% or 99% identical over a region of 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 180, 270, 360, 450, 540, 630, 720, 810, 900, 990, 1080, 1170, 1260, 1350, 1440, 1530, 1620, 1710, 1800, 1890, 1980, 2070 or more nucleotides or amino acids, or with respect to nucleic acids, if the first sequence is substantially complementary to the complement of the second sequence.

w. Subtype or Serotype

“Subtype” or “serotype”: as used herein, interchangeably, and in reference to herpes virus, means genetic variants of an herpes virus such that one subtype is recognized by an immune system apart from a different subtype.

x. Variant

“Variant” used herein with respect to a nucleic acid means (i) a portion or fragment of a referenced nucleotide sequence; (ii) the complement of a referenced nucleotide sequence or portion thereof; (iii) a nucleic acid that is substantially identical to a referenced nucleic acid or the complement thereof; or (iv) a nucleic acid that hybridizes under stringent conditions to the referenced nucleic acid, complement thereof, or a sequences substantially identical thereto.

“Variant” with respect to a peptide or polypeptide that differs in amino acid sequence by the insertion, deletion, or conservative substitution of amino acids, but retain at least one biological activity. Variant can also mean a protein with an amino acid sequence that is substantially identical to a referenced protein with an amino acid sequence that retains at least one biological activity. A conservative substitution of an amino acid, i.e., replacing an amino acid with a different amino acid of similar properties (e.g., hydrophilicity, degree and distribution of charged regions) is recognized in the art as typically involving a minor change. These minor changes can be identified, in part, by considering the hydropathic index of amino acids, as understood in the art. Kyte et al., *J. Mol. Biol.* 157:105-132 (1982). The hydropathic index of an amino acid is based on a consideration of its hydrophobicity and charge. It is known in the art that amino acids of similar hydropathic indexes can be substituted and still retain protein function. In one aspect, amino acids having hydropathic indexes of ± 2 are substituted. The hydrophilicity of amino acids can also be used to reveal substitutions that would result in proteins retaining biological function. A consideration of the hydrophilicity of amino acids in the context of a peptide permits calculation of the greatest local average hydrophilicity of that peptide, a useful measure that has been reported to correlate well with antigenicity and immunogenicity. U.S. Pat. No. 4,554,101, incorporated fully herein by reference. Substitution of amino acids having similar hydrophilicity values can result in peptides retaining biological activity, for example immunogenicity, as is understood in the art. Substitutions can be performed with amino acids having hydrophilicity values within ± 2 of each other. Both the hydrophobicity index and the hydrophilicity value of amino acids are influenced by the particular side chain of that amino acid. Consistent with that observation, amino acid substitutions that are compatible with biological function are understood to depend on the relative similarity of the amino acids, and particularly the side chains of those amino

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acids, as revealed by the hydrophobicity, hydrophilicity, charge, size, and other properties.

y. Vector

“Vector” as used herein means a nucleic acid sequence containing an origin of replication. A vector can be a vector, bacteriophage, bacterial artificial chromosome or yeast artificial chromosome. A vector can be a DNA or RNA vector. A vector can be a self-replicating extrachromosomal vector, and preferably, is a DNA plasmid.

2. Herpes Viruses, Including HCMV, HSV1, HSV2, CeHV1, and VZV, Antigens

In an aspect of the present invention, provided is a methodology to generate novel herpes virus antigens, useful across the various herpes family viruses, to increase the potential breadth of immunity elicited by each viral antigen (Ag)

Phylogenetic diversity was first examined to assess polymorphism and to aid in the production of clinically-relevant consensus amino acid sequences. Phylogenetic and molecular evolutionary analyses can be conducted using MEGA version 5 (Tamura, Peterson, Stecher, Nei, and Kumar 2011) to estimate diversity among clinically relevant and publically available herpes target protein sequences used for generating consensus vaccine Ags. Neighbor-joining phylogenetic reconstruction analysis using the bootstrap method with 1,000 bootstrap replications can be used to generate bootstrap consensus trees with radiation view.

Strategies for generating the consensus amino acid sequences for each herpes immunogen are outlined, below, in the examples. In general, consensus sequences from highly conserved herpes proteins can be used for vaccine immunogens while consensus sequences from specific, clinically relevant subgroups can be used for the highly divergent proteins.

Amino acid sequences of herpes vaccine proteins can be generated by taking the consensus of publically available (GenBank) and clinically relevant strains (passed no more than six times in tissue culture) using Vector NTI software (Invitrogen) for sequence alignment. Preferably, the antigens can be combined in a vaccine formulation as multiple vectors having single antigen or single vector having multiple antigens therein, whether 2 or more antigens. In some embodiments, more than 2 or more of the specific herpes virus antigens are present in one vaccine formulation. When multiple antigens are present on a vector (for example a DNA plasmid, e.g., pHCMV-gHgL or HSV1-gHgL) such antigens are separated by a cleavage site, preferably a furin site, e.g., SEQ ID NO:63, for the co-expression of structurally-relevant macromolecules. Genetic optimization of DNA vaccines included codon and RNA optimization for protein expression in humans and all genes were synthesized and subcloned into a modified pVAX1 mammalian expression vector (GeneArt, Regensburg, Germany or GenScript, Piscataway, N.J.).

In another aspect, provided herein are antigens capable of eliciting an immune response in a mammal against one or more herpes viruses, including HCMV, HSV1, HSV2, CeHV1, and VZV, serotypes. The antigen can comprise epitopes that make them particularly effective as immunogens against which anti-herpes virus immune responses can be induced. The herpes virus antigen can comprise the full length translation product, a variant thereof, a fragment thereof or a combination thereof. The herpes virus antigen can be a wild type sequence or a consensus sequence derived from multiple different sequences.

Various nucleic acid sequences encoding different herpes viruses, including HCMV, HSV1, HSV2, CeHV1, and VZV, proteins have been identified for use alone or in various combinations as part of a vaccine against herpes viruses that can induce an immune response against the immunogenic protein and be used in prophylactic and therapeutic vaccines. Alternatively, the proteins themselves may be used. The immunogenic proteins include gB, gM, gN, gH, gL, gO, gE, gI, gK, gC, gD, UL128, UL130, UL-131A, UL-83 (pp65), whether from HCMV, HSV1, HSV2, CeHV1, or VZV, and vaccines may comprise one or more immunogenic proteins selected from this group and/or vaccines may comprise one or more nucleic acid sequences that encode one or more immunogenic proteins selected from this group.

In view of evolutionary divergence from clinical isolates and extensive genetic differences among prevalent circulating human strains consensus amino acid sequences for each of immunogenic proteins have been generated. Consensus amino acid sequences for gB, gM, gH, gL, gE, gI, gK, gC, gD, UL128, UL130, UL-131A and UL-83 (pp65) were based upon sequences from human clinical isolates as of the beginning of 2010. Due to the great evolutionary divergence of the gN protein, the consensus sequence was generated from only one (gN-4c) of seven serotypes that represents the most sero-prevalent (gN-4). Similarly, in the case gO, a consensus amino acid sequences was generated from one (gO-5) of eight sero-types due to that particular serotypes reported linkage with the gN-4c sero-type.

In some embodiments, consensus herpes virus antigens may be provided with a signal peptide. In some embodiments, the IgE leader (SEQ ID NO:61) is linked to the N terminus. As described herein, when referring to a signal peptide linked to the N terminus of a consensus sequence, it is intended to specifically include embodiments in which the N terminal Xaa residue of the consensus sequences is replaced with a signal peptide. That is, as used herein Xaa is intended to refer to any amino acid or no amino acid. The proteins which comprise a consensus sequence set forth herein SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 85, 91, 97, 103, 111, and 113, and proteins HSV1-gH, HSV1-gL, HSV1-gC, HSV1-gD, HSV2-gH, HSV2-gL, HSV2-gC, HSV2-gD, VZV-gH, VZV-gL, VZV-gM, VZV-gN, CeHV1-gH, CeHV1-gL, CeHV1-gC, CeHV1-gD, VZV-gE, and VZV-gI, may comprise those sequences free of the N terminal Xaa.

In some embodiments, the herpes virus antigens, whether with or without a signal peptide, may comprise an antigenic tag such as the HA Tag (SEQ ID NO:62 which is induced in each of SEQ ID NOs: 42, 44, 46, 48, 50, 52, 54, 56, 58 and 60). The antigenic tags can be used to detect expression. The HA Tag is a common antigenic tag used for this purpose. Further, one or more proteins set forth above may be linked to each other to form a fusion protein. In some examples, the proteins are linked by way of a proteolytic cleavage site such as the furin site (SEQ ID NO: 63 which is included in each of SEQ ID NOs:65, 67, 69, 71, 73, 75, 87, 89, 93, 95, 99, 101, 105, 107, and 109.)

A consensus protein HCMV-gB (SEQ ID NO:2), a consensus protein HCMV-gM (SEQ ID NO:4), a consensus protein HCMV-gN (SEQ ID NO:6), a consensus protein HCMV-gH (SEQ ID NO:8), a consensus protein HCMV-gL (SEQ ID NO:10), a consensus protein HCMV-gO (SEQ ID NO:12), a consensus protein HCMV-UL128 (SEQ ID NO:14), a consensus protein HCMV-UL130 (SEQ ID NO:16), a consensus protein HCMV-UL-131A (SEQ ID NO:18), a consensus protein HCMV-UL-83 (pp65) (SEQ ID NO:20), a consensus protein HSV1-gB SEQ ID NO:85, a consensus

protein HSV1-gH (N-terminal region up to position 838 of SEQ ID NO:87), a consensus protein HSV1-gL (C-terminal region from position 846 of SEQ ID NO:87), a consensus protein HSV1-gC (N-terminal region up to position 511 of SEQ ID NO:89), a consensus protein HSV1-gD (C-terminal region from position 519 of SEQ ID NO:89), a consensus protein HSV2-gB (SEQ ID NO:91), a consensus protein HSV2-gH (N-terminal region up to position 838 of SEQ ID NO:93), a consensus protein HSV2-gL (C-terminal region from position 846 of SEQ ID NO:93), a consensus protein HSV2-gC (N-terminal region up to position 480 of SEQ ID NO:95), a consensus protein HSV2-gD (C-terminal region from position 488 of SEQ ID NO:95), a consensus protein VZV-gB (SEQ ID NO:97), a consensus protein VZV-gH (N-terminal region up to position 841 of SEQ ID NO:99), a consensus protein VZV-gL (C-terminal region from position 849 of SEQ ID NO:99), a consensus protein VZV-gM (N-terminal region up to position 435 of SEQ ID NO:101), a consensus protein VZV-gN (C-terminal region from position 443 of SEQ TD NO:101), a consensus protein CeHV1-gB (SEQ TD NO:103), a consensus protein CeHV1-gH (N-terminal region up to position 858 of SEQ ID NO:105), a consensus protein CeHV1-gL (C-terminal region from position 866 of SEQ ID NO:105), a consensus protein CeHV1-gC (N-terminal region up to position 467 of SEQ ID NO:107), a consensus protein CeHV1-gD (C-terminal region from position 475 of SEQ ID NO:107), a consensus protein VZV-gE (N-terminal region up to position 623 of SEQ ID NO:109), a consensus protein VZV-gI (C-terminal region from position 631 of SEQ ID NO:109), a consensus protein VZV-gC (SEQ ID NO:111), and a consensus protein VZV-gK (SEQ ID NO:113) are provided. Amino acid sequences were generated which comprised in each particular instance, the IgE leader sequence at the N terminus of the herpes virus immunogenic protein consensus sequences. Thus, also provided are a protein with an IgE leader linked to consensus protein HCMV-gB (SEQ ID NO:22), a protein with an IgE leader linked to consensus protein HCMV-gM (SEQ ID NO:24), a protein with an IgE leader linked to consensus protein HCMV-gN (SEQ ID NO:26), a protein with an IgE leader linked to consensus protein HCMV-gH (SEQ ID NO:28), a protein with an IgE leader linked to consensus protein HCMV-gL (SEQ ID NO:30), a protein with an IgE leader linked to consensus protein HCMV-gO (SEQ ID NO:32), a protein with an IgE leader linked to consensus protein HCMV-UL128 (SEQ ID NO:34), a protein with an IgE leader linked to consensus protein HCMV-UL130 (SEQ ID NO:36), a protein with an IgE leader linked to consensus protein HCMV-UL-131A (SEQ ID NO:38), a protein with an IgE leader linked to consensus protein HCMV-UL-83 (pp65) (SEQ ID NO:40). IgE leader used is (SEQ ID NO:62). Embodiments are also provided in which HA tags are linked at the C terminus of the consensus sequence. Accordingly, a protein with an IgE leader linked to consensus protein HCMV-gB with an HA Tag at the C terminal (SEQ ID NO:42), a protein with an IgE leader linked to consensus protein HCMV-gM (SEQ ID NO:44), a protein with an IgE leader linked to consensus protein HCMV-gN (SEQ ID NO:46), a protein with an IgE leader linked to consensus protein HCMV-gH (SEQ ID NO:48), a protein with an IgE leader linked to consensus protein HCMV-gL (SEQ ID NO:50), a protein with an IgE leader linked to consensus protein HCMV-gO (SEQ ID NO:52), a protein with an IgE leader linked to consensus protein HCMV-UL128 (SEQ ID NO:54), a protein with an IgE leader linked to consensus protein HCMV-UL130 (SEQ ID NO:56), a protein with an IgE leader linked to consensus

protein HCMV-UL-131A (SEQ TD NO:58), a protein with an IgE leader linked to consensus protein HCMV-UL-83 (pp65) (SEQ ID NO:60) are also provided. In some embodiments, nucleic acid constructs are provided in which two or more herpes virus antigens are expressed as fusion proteins linked to each other by proteolytic cleavage sites. A furin proteolytic cleavage site (SEQ ID NO:63) is an example of a proteolytic cleavage site which may link herpes virus antigens in a fusion protein expressed by a construct.

Proteins may be homologous to any of the protein sequences provided herein for each of the specific consensus antigens. Some embodiments relate to immunogenic proteins that have 95% homology to the consensus protein sequences herein. Some embodiments relate to immunogenic proteins that have 96% homology to the consensus protein sequences herein. Some embodiments relate to immunogenic proteins that have 97% homology to the consensus protein sequences herein. Some embodiments relate to immunogenic proteins that have 95% homology, or 98% homology in some instances, to the consensus protein sequences herein. Some embodiments relate to immunogenic proteins that have 99% homology to the consensus protein sequences herein.

Fragments of consensus proteins may comprise at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50% or at least 55% at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% of a consensus protein. Immunogenic fragments of any of the protein sequences provided herein for each of the specific consensus antigens may be provided. Immunogenic fragments may comprise at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50% or at least 55% at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% of any of the protein sequences provided herein for each of the specific consensus antigens.

Immunogenic fragments of proteins with amino acid sequences homologous immunogenic fragments of any of the protein sequences provided herein for each of the specific consensus antigens may be provided. Such immunogenic fragments may comprise at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50% or at least 55% at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% of proteins that are 95% homologous to any of the protein sequences provided herein for each of the specific consensus antigens. Some embodiments relate to immunogenic fragments that have 96% homology to the immunogenic fragments of consensus protein sequences herein. Some embodiments relate to immunogenic fragments that have 97% homology to the immunogenic fragments of consensus protein sequences herein. Some embodiments relate to immunogenic fragments that have 95% homology, or 98% homology in some instances, to the immunogenic fragments of consensus protein sequences herein. Some embodiments relate to immunogenic fragments that have 99% homology to the immunogenic fragments of consensus protein sequences herein.

3. Genetic Sequences, Constructs and Plasmids

Nucleic acid sequences encoding the SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ TD NO:8, SEQ TD NO:10,

SEQ TD NO:12, SEQ TD NO:14, SEQ TD NO:16, SEQ TD NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, a consensus protein HSV1-gB SEQ TD NO:85, a consensus protein HSV1-gH (N-terminal region up to position 838 of SEQ ID NO:87), a consensus protein HSV1-gL (C-terminal region from position 846 of SEQ ID NO:87), a consensus protein HSV1-gC (N-terminal region up to position 511 of SEQ ID NO:89), a consensus protein HSV1-gD (C-terminal region from position 519 of SEQ ID NO:89), a consensus protein HSV2-gB (SEQ ID NO:91), a consensus protein HSV2-gH (N-terminal region up to position 838 of SEQ ID NO:93), a consensus protein HSV2-gL (C-terminal region from position 846 of SEQ ID NO:93), a consensus protein HSV2-gC (N-terminal region up to position 480 of SEQ ID NO:95), a consensus protein HSV2-gD (C-terminal region from position 488 of SEQ ID NO:95), a consensus protein VZV-gB (SEQ ID NO:97), a consensus protein VZV-gH (N-terminal region up to position 841 of SEQ ID NO:99), a consensus protein VZV-gL (C-terminal region from position 849 of SEQ ID NO:99), a consensus protein VZV-gM (N-terminal region up to position 435 of SEQ ID NO:101), a consensus protein VZV-gN (C-terminal region from position 443 of SEQ ID NO:101), a consensus protein CeHV1-gB (SEQ ID NO:103), a consensus protein CeHV1-gH (N-terminal region up to position 858 of SEQ ID NO:105), a consensus protein CeHV1-gL (C-terminal region from position 866 of SEQ ID NO:105), a consensus protein CeHV1-gC (N-terminal region up to position 467 of SEQ ID NO:107), a consensus protein CeHV1-gD (C-terminal region from position 475 of SEQ ID NO:107), a consensus protein VZV-gE (N-terminal region up to position 623 of SEQ ID NO:109), a consensus protein VZV-gI (C-terminal region from position 631 of SEQ ID NO:109), a consensus protein VZV-gC (SEQ ID NO:111), and a consensus protein VZV-gK (SEQ ID NO:113) as well as homologous protein, immunogenic fragment and immunogenic fragments of homologous proteins can be generated routinely. Thus, nucleic acid molecules that encode immunogenic proteins that have up to 95% homology to a consensus sequence, up to 96% homology to a consensus sequence, up to 96% homology to a consensus sequence, up to 97% homology to a consensus sequence, up to 98% homology to a consensus sequence and up to 99% may be provided. Likewise, nucleic acid sequences encoding the immunogenic fragments set forth herein and the immunogenic fragments of protein homologous to the proteins set forth herein are also provided.

Nucleic acid molecules encoding the consensus amino acid sequences were generated. Vaccines may comprise one or more nucleic acid sequences that encode one or more of the consensus versions of the immunogenic proteins selected from this group of sequences generated to optimize stability and expression in humans. Nucleic acid sequence encoding consensus protein HCMV-gB (SEQ ID NO:1), nucleic acid sequence encoding consensus protein HCMV-gM (SEQ ID NO:3), nucleic acid sequence encoding consensus protein HCMV-gN (SEQ ID NO:5), nucleic acid sequence encoding consensus protein HCMV-gH (SEQ ID NO:7), nucleic acid sequence encoding consensus protein HCMV-gL (SEQ ID NO:9), nucleic acid sequence encoding consensus protein HCMV-gO (SEQ ID NO:11), nucleic acid sequence encoding consensus protein HCMV-UL128 (SEQ ID NO:13),

nucleic acid sequence encoding consensus protein HCMV-UL130 (SEQ ID NO:15), nucleic acid sequence encoding consensus protein HCMV-UL-131A (SEQ ID NO:17), nucleic acid sequence encoding consensus protein HCMV-UL-83 (pp65) (SEQ ID NO:19), nucleic acid sequence encoding consensus protein HSV1-gB (SEQ ID NO:86), nucleic acid sequence encoding consensus protein HSV1-gH (N-terminal portion of SEQ ID NO:88, before furin site), nucleic acid sequence encoding consensus protein HSV1-gL (C-terminal portion of SEQ ID NO:88, after furin site), nucleic acid sequence encoding consensus protein HSV1-gC (N-terminal portion of SEQ ID NO:90, prior to furin site), nucleic acid sequence encoding consensus protein HSV1-gD (C-terminal portion of SEQ ID NO:90, after furin site), nucleic acid sequence encoding consensus protein HSV2-gB (SEQ ID NO:92), nucleic acid sequence encoding consensus protein HSV2-gH (N-terminal portion of SEQ ID NO:94, prior to furin site), nucleic acid sequence encoding consensus protein HSV2-gL (C-terminal portion of SEQ ID NO:94, after furin site), nucleic acid sequence encoding consensus protein HSV2-gC (N-terminal portion of SEQ ID NO:96, prior to furin site), nucleic acid sequence encoding consensus protein HSV2-gD (C-terminal portion of SEQ ID NO:96, after furin site), nucleic acid sequence encoding consensus protein VZV-gB (SEQ ID NO:98), nucleic acid sequence encoding consensus protein VZV-gH (N-terminal portion of SEQ ID NO:100, prior to furin site), nucleic acid sequence encoding consensus protein VZV-gL (C-terminal portion of SEQ ID NO:100, after furin site), nucleic acid sequence encoding consensus protein VZV-gM (N-terminal portion of SEQ ID NO:102, prior to furin site), nucleic acid sequence encoding consensus protein VZV-gN (C-terminal portion of SEQ ID NO:102, after furin site), nucleic acid sequence encoding consensus protein CeHV1-gB (SEQ ID NO:104), nucleic acid sequence encoding consensus protein CeHV1-gH (N-terminal portion of SEQ ID NO:106, prior to furin site), nucleic acid sequence encoding consensus protein CeHV1-gL (C-terminal portion of SEQ ID NO:106, after furin site), nucleic acid sequence encoding consensus protein CeHV1-gC (N-terminal portion of SEQ ID NO:108, prior to furin site), nucleic acid sequence encoding consensus protein CeHV1-gD (C-terminal portion of SEQ ID NO:108, after furin site), nucleic acid sequence encoding consensus protein VZV-gE (N-terminal portion of SEQ ID NO:110, prior to furin site), nucleic acid sequence encoding consensus protein VZV-gI (C-terminal portion of SEQ ID NO:110, after furin site), nucleic acid sequence encoding consensus protein VZV-gC (SEQ ID NO:112), and nucleic acid sequence encoding consensus protein VZV-gK (SEQ ID NO:114) are provided herein. In addition, nucleic acid sequences incorporating coding sequence for the IgE leader at the 5' end of the optimized, consensus encoding nucleic acid sequence were generated which encoded proteins having the IgE leader sequence at the N terminus of the consensus amino acid sequence. The nucleic acid sequence encoding IgE leader linked to consensus protein HCMV-gB (SEQ ID NO:21), nucleic acid sequence encoding IgE leader linked to consensus protein HCMV-gM (SEQ ID NO:23), nucleic acid sequence encoding IgE leader linked to consensus protein HCMV-gN (SEQ ID NO:25), nucleic acid sequence encoding IgE leader linked to consensus protein HCMV-gH (SEQ ID NO:27), nucleic acid sequence encoding IgE leader linked to consensus protein HCMV-gL (SEQ ID NO:29), nucleic acid sequence encoding IgE leader linked to consensus protein HCMV-gO (SEQ ID NO:31), nucleic acid sequence encoding IgE leader linked to consensus protein HCMV-UL128 (SEQ ID NO:33), nucleic

acid sequence encoding IgE leader linked to consensus protein HCMV-UL130 (SEQ ID NO:35), nucleic acid sequence encoding IgE leader linked to consensus protein HCMV-UL-131A (SEQ ID NO:37), nucleic acid sequence encoding IgE leader linked to consensus protein HCMV-UL-83 (pp65) (SEQ ID NO:39), are provided. The nucleic acid sequence encoding IgE leader (DNA encoding SEQ ID NO:61). The nucleic acid sequence encoding IgE leader linked to consensus protein HCMV-gB with an HA Tag at the C terminus (SEQ ID NO:42), nucleic acid sequence encoding IgE leader linked to consensus protein HCMV-gM with an HA Tag at the C terminus (SEQ ID NO:43), nucleic acid sequence encoding IgE leader linked to consensus protein HCMV-gN with an HA Tag at the C terminus (SEQ ID NO:45), nucleic acid sequence encoding IgE leader linked to consensus protein HCMV-gH with an HA Tag at the C terminus (SEQ ID NO:47), nucleic acid sequence encoding IgE leader linked to consensus protein HCMV-gL with an HA Tag at the C terminus (SEQ ID NO:49), nucleic acid sequence encoding IgE leader linked to consensus protein HCMV-gO with an HA Tag at the C terminus (SEQ ID NO:51), nucleic acid sequence encoding IgE leader linked to consensus protein HCMV-UL128 with an HA Tag at the C terminus (SEQ ID NO:53), nucleic acid sequence encoding IgE leader linked to consensus protein HCMV-UL130 with an HA Tag at the HCMV-C terminus (SEQ ID NO:55), nucleic acid sequence encoding IgE leader linked to consensus protein HCMV-UL-131A with an HA Tag at the C terminus (SEQ ID NO:57), nucleic acid sequence encoding IgE leader linked to consensus protein HCMV-UL-83 (pp65) with an HA Tag at the C terminus (SEQ ID NO:59), are provided.

Some embodiments relate to nucleic acid molecules that encode immunogenic proteins that have 95% homology to the nucleic acid coding sequences herein. Some embodiments relate to nucleic acid molecules that encode immunogenic proteins that have 96% homology to the nucleic acid coding sequences herein. Some embodiments relate to nucleic acid molecules that encode immunogenic proteins that have 97% homology to the nucleic acid coding sequences herein. Some embodiments relate to nucleic acid molecules that encode immunogenic proteins that have 98% homology to the nucleic acid coding sequences herein. Some embodiments relate to nucleic acid molecules that encode immunogenic proteins that have 99% homology to the nucleic acid coding sequences herein. In some embodiments, the nucleic acid molecules with coding sequences disclosed herein that are homologous to a coding sequence of a consensus protein disclosed herein include sequences encoding an IgE leader sequence linked to the 5' end of the coding sequence encoding the homologous protein sequences disclosed herein.

Some embodiments relate to fragments of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:86, nucleic acid sequence encoding consensus protein HSV1-gH (N-terminal portion of SEQ ID NO:88, before furin site), nucleic acid sequence encoding consensus protein HSV1-gL (C-terminal portion of SEQ ID NO:88, after furin site), nucleic acid sequence encoding consensus protein HSV1-gC (N-terminal portion of SEQ ID

NO:90, prior to furin site), nucleic acid sequence encoding consensus protein HSV1-gD (C-terminal portion of SEQ ID NO:90, after furin site), SEQ ID NO:92, nucleic acid sequence encoding consensus protein HSV2-gH (N-terminal portion of SEQ ID NO:94, prior to furin site), nucleic acid sequence encoding consensus protein HSV2-gL (C-terminal portion of SEQ ID NO:94, after furin site), nucleic acid sequence encoding consensus protein HSV2-gC (N-terminal portion of SEQ ID NO:96, prior to furin site), nucleic acid sequence encoding consensus protein HSV2-gD (C-terminal portion of SEQ ID NO:96, after furin site), SEQ ID NO:98, nucleic acid sequence encoding consensus protein VZV-gH (N-terminal portion of SEQ ID NO:100, prior to furin site), nucleic acid sequence encoding consensus protein VZV-gL (C-terminal portion of SEQ ID NO:100, after furin site), nucleic acid sequence encoding consensus protein VZV-gM (N-terminal portion of SEQ TD NO:102, prior to furin site), nucleic acid sequence encoding consensus protein VZV-gN (C-terminal portion of SEQ ID NO:102, after furin site), SEQ ID NO:104, nucleic acid sequence encoding consensus protein CeHV1-gH (N-terminal portion of SEQ ID NO:106, prior to furin site), nucleic acid sequence encoding consensus protein CeHV1-gL (C-terminal portion of sEQ ID NO:106, after furin site), nucleic acid sequence encoding consensus protein CeHV1-gC (N-terminal portion of SEQ ID NO:108, prior to furin site), nucleic acid sequence encoding consensus protein CeHV1-gD (C-terminal portion of SEQ ID NO:108, after furin site), nucleic acid sequence encoding consensus protein VZV-gE (N-terminal portion of SEQ ID NO:110, prior to furin site), nucleic acid sequence encoding consensus protein VZV-gI (C-terminal portion of SEQ ID NO:110, after furin site), SEQ ID NO:112, and SEQ ID NO:114. Fragments may be at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50% or at least 55% at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% of any of the nucleotide sequences provided herein for each of the specific consensus antigens. Fragments may be at least 95%, at least 96%, at least 97% at least 98% or at least 99% homologous to fragments of any of the nucleotide sequences provided herein for each of the specific consensus antigens.

Provided herein are genetic constructs that can comprise a nucleic acid sequence that encodes the herpes virus antigen disclosed herein including consensus protein sequences, sequences homologous to consensus protein sequences, fragments of consensus protein sequences and sequences homologous to fragments of consensus protein sequences. The genetic construct can be present in the cell as a functioning extrachromosomal molecule. The genetic construct can be linear minichromosome including centromere, telomers or plasmids or cosmids.

The genetic construct can also be part of a genome of a recombinant viral vector, including recombinant adenovirus, recombinant adenovirus associated virus and recombinant vaccinia. The genetic construct can be part of the genetic material in attenuated live microorganisms or recombinant microbial vectors which live in cells.

The genetic constructs can comprise regulatory elements for gene expression of the coding sequences of the nucleic acid. The regulatory elements can be a promoter, an enhancer an initiation codon, a stop codon, or a polyadenylation signal.

The nucleic acid sequences may make up a genetic construct that can be a vector. The vector can be capable of expressing an antigen in the cell of a mammal in a quantity

effective to elicit an immune response in the mammal. The vector can be recombinant. The vector can comprise heterologous nucleic acid encoding the antigen. The vector can be a plasmid. The vector can be useful for transfecting cells with nucleic acid encoding an antigen, which the transformed host cell is cultured and maintained under conditions wherein expression of the antigen takes place.

In some embodiments, coding sequences for one antigen may be provided on a single vector.

In some embodiments, coding sequences for two or more different antigens may be provided on a single vector. In some embodiments, the coding sequences may have separate promoters controlling expression. In some embodiments, the coding sequences may have a single promoters controlling expression with an IRES sequence separating coding sequence. The presence of the IRES sequence results in the separate translation of the transcription product. In some embodiments, the coding sequences may have a single promoters controlling expression with coding sequence encoding a proteolytic cleavage peptide sequence separating coding sequences of the antigens. A single translation product is produced which is then processed by the protease that recognizes the protease cleavage site to generate separate protein molecules. The protease cleave sites used is typically recognized by a protease endogenously present in the cell where expression occurs. In some embodiments, a separate coding sequence for a protease may be included to provide for the production of the protease needed to process the polyprotein translation product. In some embodiment, vectors comprise coding sequences for one, two, three, four or more HCMV antigens, HSV1 antigens, HSV2 antigens, VZV antigens, or CeHV1 antigens.

In some embodiments, coding sequences for HCMV antigens gM and gN are included on the same vector. In some embodiments, coding sequences for HCMV antigens consensus gM and consensus gN4-c are included on the same vector. In some embodiments, coding sequences for HCMV antigens gM and gN are included on the same vector and are under control of a single promoter. In some embodiments, coding sequences for HCMV antigens consensus gM and consensus gN4-c are included on the same vector and are under control of a single promoter. In some embodiments, coding sequences for HCMV antigens gM and gN are included on the same vector, under control of a single promoter and linked with a coding sequence for a proteolytic cleavage site. In some embodiments, coding sequences for HCMV antigens consensus gM and consensus gN4-c are included on the same vector, are under control of a single promoter and linked with a coding sequence for a proteolytic cleavage site. In some embodiments, coding sequences for HCMV antigens gH and gL are included on the same vector. In some embodiments, coding sequences for HCMV antigens consensus gH and consensus gL are included on the same vector. In some embodiments, coding sequences for HCMV antigens gH and gL are included on the same vector and are under control of a single promoter. In some embodiments, coding sequences for HCMV antigens consensus gH and consensus gL are included on the same vector and are under control of a single promoter. In some embodiments, coding sequences for HCMV antigens gH and gL are included on the same vector, under control of a single promoter and linked with a coding sequence for a proteolytic cleavage site. In some embodiments, coding sequences for HCMV antigens consensus gH and consensus gL are included on the same vector, are under control of a single promoter and linked with a coding sequence for a proteolytic cleavage site.

In some embodiments, coding sequences for HCMV antigens/chaperone proteins UL128, UL130 and UL-131A are included on the same vector. In some embodiments, coding sequences for HCMV antigens/chaperone proteins consensus UL128, consensus UL130 and consensus UL-131A are included on the same vector. In some embodiments, coding sequences for HCMV antigens/chaperone proteins UL128, UL130 and UL-131A are included on the same vector and are under control of a single promoter. In some embodiments, coding sequences for HCMV antigens/chaperone proteins consensus UL128, consensus UL130 and consensus UL-131A are included on the same vector and are under control of a single promoter. In some embodiments, coding sequences for HCMV antigens/chaperone proteins UL128, UL130 and UL-131A are included on the same vector, under control of a single promoter and linked with a coding sequence for a proteolytic cleavage site. In some embodiments, coding sequences for HCMV antigens/chaperone proteins consensus UL128, consensus UL130 and consensus UL-131A are included on the same vector, are under control of a single promoter and linked with a coding sequence for a proteolytic cleavage site.

In some embodiments, coding sequences for HSV1 antigens gH and gL are included on the same vector, and in some cases under the control of a single promoter, and in some cases linked together with a coding sequence for a proteolytic cleavage site, preferably furin cleavage site. In some embodiments, coding sequences for HSV1 antigens gC and gD are included on the same vector, and in some cases under the control of a single promoter, and in some cases linked together with a coding sequence for a proteolytic cleavage site, preferably furin cleavage site. In some embodiments, coding sequences for HSV2 antigens gH and gL are included on the same vector, and in some cases under the control of a single promoter, and in some cases linked together with a coding sequence for a proteolytic cleavage site, preferably furin cleavage site. In some embodiments, coding sequences for HSV2 antigens gC and gD are included on the same vector, and in some cases under the control of a single promoter, and in some cases linked together with a coding sequence for a proteolytic cleavage site, preferably furin cleavage site. In some embodiments, coding sequences for VZV antigens gH and gL are included on the same vector, and in some cases under the control of a single promoter, and in some cases linked together with a coding sequence for a proteolytic cleavage site, preferably furin cleavage site. In some embodiments, coding sequences for VZV antigens gM and gN are included on the same vector, and in some cases under the control of a single promoter, and in some cases linked together with a coding sequence for a proteolytic cleavage site, preferably furin cleavage site. In some embodiments, coding sequences for CeHV1 antigens gH and gL are included on the same vector, and in some cases under the control of a single promoter, and in some cases linked together with a coding sequence for a proteolytic cleavage site, preferably furin cleavage site. In some embodiments, coding sequences for CeHV1 antigens gC and gD are included on the same vector, and in some cases under the control of a single promoter, and in some cases linked together with a coding sequence for a proteolytic cleavage site, preferably furin cleavage site. In some embodiments, coding sequences for VZV antigens gE and gI are included on the same vector, and in some cases under the control of a single promoter, and in some cases linked together with a coding sequence for a proteolytic cleavage site, preferably furin cleavage site.

Coding sequences for any protein disclosed herein may be provided as a single coding sequence on a single. Likewise, coding sequences for any combination of different proteins disclosed herein may be provided on a single vector, either with its own promoter, linked with an IRES sequence or as a single coding sequence of a polyprotein in which the individual proteins are linked with proteolytic cleavage sites.

In each and every instance set forth herein, coding sequences may be optimized for stability and high levels of expression. In some instances, codons are selected to reduce secondary structure formation of the RNA such as that formed due to intramolecular bonding.

The vector can comprise heterologous nucleic acid encoding an antigen and can further comprise an initiation codon, which can be upstream of the antigen coding sequence, and a stop codon, which can be downstream of the antigen coding sequence. The initiation and termination codon can be in frame with the antigen coding sequence. The vector can also comprise a promoter that is operably linked to the antigen coding sequence. The promoter operably linked to the antigen coding sequence can be a promoter from simian virus 40 (SV40), a mouse mammary tumor virus (MMTV) promoter, a human immunodeficiency virus (HIV) promoter such as the bovine immunodeficiency virus (BIV) long terminal repeat (LTR) promoter, a Moloney virus promoter, an avian leukosis virus (ALV) promoter, a cytomegalovirus (CMV) promoter such as the CMV immediate early promoter, Epstein Barr virus (EBV) promoter, or a Rous sarcoma virus (RSV) promoter. The promoter can also be a promoter from a human gene such as human actin, human myosin, human hemoglobin, human muscle creatine, or human metallothionein. The promoter can also be a tissue specific promoter, such as a muscle or skin specific promoter, natural or synthetic. Examples of such promoters are described in US patent application publication no. US20040175727, the contents of which are incorporated herein in its entirety.

The vector can also comprise a polyadenylation signal, which can be downstream of the herpes antigen coding sequence. The polyadenylation signal can be a SV40 polyadenylation signal, LTR polyadenylation signal, bovine growth hormone (bGH) polyadenylation signal, human growth hormone (hGH) polyadenylation signal, or human β -globin polyadenylation signal. The SV40 polyadenylation signal can be a polyadenylation signal from a pCEP4 vector (Invitrogen, San Diego, Calif.).

The vector can also comprise an enhancer upstream of the consensus herpes antigen coding sequence. The enhancer can be necessary for DNA expression. The enhancer can be human actin, human myosin, human hemoglobin, human muscle creatine or a viral enhancer such as one from CMV, HA, RSV or EBV. Polynucleotide function enhances are described in U.S. Pat. Nos. 5,593,972, 5,962,428, and WO94/016737, the contents of each are fully incorporated by reference.

The vector can also comprise a mammalian origin of replication in order to maintain the vector extrachromosomally and produce multiple copies of the vector in a cell. The vector can be pVAX1, pCEP4 or pREP4 from Invitrogen (San Diego, Calif.), which can comprise the Epstein Barr virus origin of replication and nuclear antigen EBNA-1 coding region, which can produce high copy episomal replication without integration. The vector can be pVAX1 or a pVax1 variant (FIG. 1) with changes such as those included in SEQ ID NO:76. The variant pVax1 plasmid is a 2998 basepair variant of the backbone vector plasmid

pVAX1 (Invitrogen, Carlsbad Calif.). The CMV promoter is located at bases 137-724. The T7 promoter/priming site is at bases 664-683. Multiple cloning sites are at bases 696-811. Bovine GH polyadenylation signal is at bases 829-1053. The Kanamycin resistance gene is at bases 1226-2020. The pUC origin is at bases 2320-2993. Based upon the sequence of pVAX1 available from Invitrogen, the following mutations were found in the sequence of pVAX1 that was used as the backbone for plasmids 1-6 set forth herein:

C>G 241 in CMV promoter

C>T 1942 backbone, downstream of the bovine growth hormone polyadenylation signal (bGHpolyA)

A>—2876 backbone, downstream of the Kanamycin gene

C>T 3277 in pUC origin of replication (Ori) high copy number mutation (see Nucleic Acid Research 1985)

G>C 3753 in very end of pUC On upstream of RNaseH site

Base pairs 2, 3 and 4 are changed from ACT to CTG in backbone, upstream of CMV promoter. The backbone of the vector can be pAV0242. The vector can be a replication defective adenovirus type 5 (Ad5) vector.

The vector can also comprise a regulatory sequence, which can be well suited for gene expression in a mammalian or human cell into which the vector is administered. The consensus herpes antigen coding sequence can comprise a codon, which can allow more efficient transcription of the coding sequence in the host cell.

The vector can be pSE420 (Invitrogen, San Diego, Calif.), which can be used for protein production in *Escherichia coli* (*E. coli*). The vector can also be pYES2 (Invitrogen, San Diego, Calif.), which can be used for protein production in *Saccharomyces cerevisiae* strains of yeast. The vector can also be of the MAXBAC™ complete baculovirus expression system (Invitrogen, San Diego, Calif.), which can be used for protein production in insect cells. The vector can also be pcDNA1 or pcDNA3 (Invitrogen, San Diego, Calif.), which maybe used for protein production in mammalian cells such as Chinese hamster ovary (CHO) cells. The vector can be expression vectors or systems to produce protein by routine techniques and readily available starting materials including Sambrook et al., *Molecular Cloning a Laboratory Manual*, Second Ed., Cold Spring Harbor (1989), which is incorporated fully by reference.

4. Pharmaceutical Compositions

Provided herein are pharmaceutical compositions according to the present invention which comprise about 1 nanogram to about 10 mgs of DNA. In some embodiments, pharmaceutical compositions according to the present invention comprise from between: 1) at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95 or 100 nanograms, or at least 1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 205, 210, 215, 220, 225, 230, 235, 240, 245, 250, 255, 260, 265, 270, 275, 280, 285, 290, 295, 300, 305, 310, 315, 320, 325, 330, 335, 340, 345, 350, 355, 360, 365, 370, 375, 380, 385, 390, 395, 400, 405, 410, 415, 420, 425, 430, 435, 440, 445, 450, 455, 460, 465, 470, 475, 480, 485, 490, 495, 500, 605, 610, 615, 620, 625, 630, 635, 640, 645, 650, 655, 660, 665, 670, 675, 680, 685, 690, 695, 700, 705, 710, 715, 720, 725, 730, 735, 740, 745, 750, 755, 760, 765, 770, 775, 780, 785, 790, 795, 800, 805, 810, 815, 820, 825, 830, 835, 840, 845, 850, 855, 860, 865, 870, 875, 880, 885, 890, 895, 900, 905, 910, 915, 920, 925, 930, 935, 940,

945, 950, 955, 960, 965, 970, 975, 980, 985, 990, 995 or 1000 micrograms, or at least 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5, 5.5, 6, 6.5, 7, 7.5, 8, 8.5, 9, 9.5 or 10 mg or more; and 2) up to and including 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95 or 100 nanograms, or up to and including 1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 205, 210, 215, 220, 225, 230, 235, 240, 245, 250, 255, 260, 265, 270, 275, 280, 285, 290, 295, 300, 305, 310, 315, 320, 325, 330, 335, 340, 345, 350, 355, 360, 365, 370, 375, 380, 385, 390, 395, 400, 405, 410, 415, 420, 425, 430, 435, 440, 445, 450, 455, 460, 465, 470, 475, 480, 485, 490, 495, 500, 605, 610, 615, 620, 625, 630, 635, 640, 645, 650, 655, 660, 665, 670, 675, 680, 685, 690, 695, 700, 705, 710, 715, 720, 725, 730, 735, 740, 745, 750, 755, 760, 765, 770, 775, 780, 785, 790, 795, 800, 805, 810, 815, 820, 825, 830, 835, 840, 845, 850, 855, 860, 865, 870, 875, 880, 885, 890, 895, 900, 905, 910, 915, 920, 925, 930, 935, 940, 945, 950, 955, 960, 965, 970, 975, 980, 985, 990, 995, or 1000 micrograms, or up to and including 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5, 5.5, 6, 6.5, 7, 7.5, 8, 8.5, 9, 9.5 or 10 mgs. In some embodiments, pharmaceutical compositions according to the present invention comprise about 5 nanograms to about 10 mgs of DNA. In some embodiments, pharmaceutical compositions according to the present invention comprise about 25 nanograms to about 5 mgs of DNA. In some embodiments, the pharmaceutical compositions contain about 50 nanograms to about 1 mg of DNA. In some embodiments, the pharmaceutical compositions contain about 0.1 to about 500 micrograms of DNA. In some embodiments, the pharmaceutical compositions contain about 1 to about 350 micrograms of DNA. In some embodiments, the pharmaceutical compositions contain about 5 to about 250 micrograms of DNA. In some embodiments, the pharmaceutical compositions contain about 10 to about 200 micrograms of DNA. In some embodiments, the pharmaceutical compositions contain about 15 to about 150 micrograms of DNA. In some embodiments, the pharmaceutical compositions contain about 20 to about 100 micrograms of DNA. In some embodiments, the pharmaceutical compositions contain about 25 to about 75 micrograms of DNA. In some embodiments, the pharmaceutical compositions contain about 30 to about 50 micrograms of DNA. In some embodiments, the pharmaceutical compositions contain about 35 to about 40 micrograms of DNA. In some embodiments, the pharmaceutical compositions contain about 100 to about 200 microgram DNA. In some embodiments, the pharmaceutical compositions comprise about 10 microgram to about 100 micrograms of DNA. In some embodiments, the pharmaceutical compositions comprise about 20 micrograms to about 80 micrograms of DNA. In some embodiments, the pharmaceutical compositions comprise about 25 micrograms to about 60 micrograms of DNA. In some embodiments, the pharmaceutical compositions comprise about 30 nanograms to about 50 micrograms of DNA. In some embodiments, the pharmaceutical compositions comprise about 35 nanograms to about 45 micrograms of DNA. In some preferred embodiments, the pharmaceutical compositions contain about 0.1 to about 500 micrograms of DNA. In some preferred embodiments, the pharmaceutical compositions contain about 1 to about 350 micrograms of DNA. In some preferred embodiments, the pharmaceutical compositions contain about 25 to about 250 micrograms of DNA. In some preferred embodiments, the pharmaceutical compositions contain about 100 to about 200 microgram DNA.

The pharmaceutical compositions according to the present invention are formulated according to the mode of administration to be used. In cases where pharmaceutical compositions are injectable pharmaceutical compositions, they are sterile, pyrogen free and particulate free. An isotonic formulation is preferably used. Generally, additives for isotonicity can include sodium chloride, dextrose, mannitol, sorbitol and lactose. In some cases, isotonic solutions such as phosphate buffered saline are preferred. Stabilizers include gelatin and albumin. In some embodiments, a vasoconstriction agent is added to the formulation.

Preferably the pharmaceutical composition is a vaccine, and more preferably a DNA vaccine.

Provided herein is a vaccine capable of generating in a mammal an immune response against herpes virus antigens. The vaccine can comprise the genetic construct as discussed above. The vaccine can comprise a plurality of the vectors each directed to one or more herpes virus antigens. The vaccine may comprise one or more nucleic acid sequences that encode one or more consensus herpes virus antigens. When the vaccine comprises more than one consensus herpes virus nucleic acid sequences, all such sequences may be present on a single nucleic acid molecule or each such sequences may be present on a different nucleic acid molecule. Alternatively, vaccines that comprise more than one consensus herpes virus nucleic acid sequences may comprise nucleic acid molecules with a single consensus herpes virus-nucleic acid sequence and nucleic acid molecules with more than one consensus herpes virus nucleic acid sequences. In addition, vaccines comprising one or more consensus herpes virus nucleic acid sequences may further comprise coding sequences for one or more herpes virus antigens.

Vaccines may comprise one or more of the consensus versions of the immunogenic proteins set forth herein and/or vaccines may comprise one or more nucleic acid sequences that encode one or more of the consensus versions of the immunogenic proteins selected from this group. Vaccines may comprise one or more of the consensus versions of the immunogenic proteins set forth herein in combination with other immunogenic herpes virus proteins with sequences other than the consensus sequences disclosed herein including wild type sequences and/or vaccines may comprise one or more nucleic acid sequences that encode one or more of the consensus versions of the immunogenic proteins selected from this group in combination with nucleic acid molecules that encode other immunogenic herpes virus proteins with sequences other than the consensus sequences disclosed herein including wild type sequences.

While not being bound by scientific theory, a vaccine that can be used to elicit an immune response (humoral, cellular, or both) broadly against herpes virus may comprise one or more of the following nucleic acid sequences that encodes one or more herpes virus antigens selected from the group consisting of: a) for HCMV: consensus gB, consensus gM, consensus gN4-c, consensus gH, consensus gL, consensus gO-5, consensus UL128, consensus UL130, consensus UL131a, consensus UL83; b) for HSV1: consensus gB, consensus gH, consensus gL, consensus gC, and consensus gD; c) for HSV2: consensus gB, consensus gH, consensus gL, consensus gC, and consensus gD; d) for CeHV1: consensus gB, consensus gH, consensus gL, consensus gC, and consensus gD; and e) for VZV: consensus gB, consensus gH, consensus gL, consensus gC, and consensus gK, consensus gM, consensus gN, consensus gE, and consensus gI; proteins homologous to any of the consensus herpes antigens, above; fragments of any of the consensus herpes antigens,

above; and fragments of proteins homologous to any of the consensus herpes antigens, above. In addition, vaccines comprising any of the above nucleic acid sequences may further comprise one or more nucleic acid sequences encoding one or more proteins selected from the group consisting of: a) for HCMV: gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, and UL83; b) for HSV1: gB, gH, gL, gC, and gD; c) for HSV2: gB, gH, gL, gC, and gD; d) for CeHV1: gB, gH, gL, gC, and gD; and e) for VZV: gB, gH, gL, gC, gK, gM, gN, gE, and gI. Alternatively, vaccines may comprise one or more protein molecules instead of or in addition to any coding sequence set forth above.

Vaccines may comprise coding sequences for consensus protein gB (SEQ ID NO:2 and/or SEQ ID NO:22 and/or SEQ ID NO:42). Vaccines may comprise coding sequences for consensus protein gB (SEQ ID NO:2 and/or SEQ ID NO:22 and/or SEQ ID NO:42) plus one or more coding sequences for gM, gN, gH, gL, gO, UL128, UL130, UL131a and UL83. Vaccines may comprise coding sequences for consensus protein gB (SEQ ID NO:2 and/or SEQ ID NO:22 and/or SEQ ID NO:42). plus coding sequences for one or more of (SEQ ID NO:4), (SEQ ID NO:6), (SEQ ID NO:8), (SEQ ID NO:10), (SEQ ID NO:12), (SEQ ID NO:14), (SEQ ID NO:16), (SEQ ID NO:18), (SEQ ID NO:20), (SEQ ID NO:24), (SEQ ID NO:26), (SEQ ID NO:28), (SEQ ID NO:30), (SEQ ID NO:32), (SEQ ID NO:34), (SEQ ID NO:36), (SEQ ID NO:38), (SEQ ID NO:40), (SEQ ID NO:44), (SEQ ID NO:46), (SEQ ID NO:48), (SEQ ID NO:50), (SEQ ID NO:52), (SEQ ID NO:54), (SEQ ID NO:56), (SEQ ID NO:58), (SEQ ID NO:60).

Vaccines may comprise specific coding sequences encoding consensus protein gB SEQ ID NO:1 and/or SEQ ID NO:21 and/or SEQ ID NO:41. Vaccines may comprise consensus protein gB coding sequences SEQ ID NO:1 and/or SEQ ID NO:21 and/or SEQ ID NO:41 plus one or more coding sequences for gM, gN, gH, gL, gO, UL128, UL130, UL131a and UL83. Vaccines may comprise gB coding sequences (SEQ ID NO:1 and/or SEQ ID NO:21 and/or SEQ ID NO:41). plus consensus protein coding sequences (SEQ ID NO:3), (SEQ ID NO:5), (SEQ ID NO:7), (SEQ ID NO:9), (SEQ ID NO:11), (SEQ ID NO:13), (SEQ ID NO:15), (SEQ ID NO:17), (SEQ ID NO:19), (SEQ ID NO:23), (SEQ ID NO:25), (SEQ ID NO:27), (SEQ ID NO:29), (SEQ ID NO:31), (SEQ ID NO:33), (SEQ ID NO:35), (SEQ ID NO:37), (SEQ ID NO:39), (SEQ ID NO:43), (SEQ ID NO:45), (SEQ ID NO:47), (SEQ ID NO:49), (SEQ ID NO:51), (SEQ ID NO:53), (SEQ ID NO:55), (SEQ ID NO:57), and (SEQ ID NO:59).

Vaccines may comprise coding sequences for consensus protein gM (SEQ ID NO:4 and/or SEQ ID NO:24 and/or SEQ ID NO:44). Vaccines may comprise coding sequences for consensus protein gM (SEQ ID NO:4 and/or SEQ ID NO:24 and/or SEQ ID NO:44) plus one or more coding sequences for gB, gN, gH, gL, gO, UL128, UL130, UL131a and UL83. Vaccines may comprise coding sequences for consensus protein gM (SEQ ID NO:4 and/or SEQ ID NO:24 and/or SEQ ID NO:44). plus coding sequences for one or more of (SEQ ID NO:2), (SEQ ID NO:6), (SEQ ID NO:8), (SEQ ID NO:10), (SEQ ID NO:12), (SEQ ID NO:14), (SEQ ID NO:16), (SEQ ID NO:18), (SEQ ID NO:20), (SEQ ID NO:22), (SEQ ID NO:26), (SEQ ID NO:28), (SEQ ID NO:30), (SEQ ID NO:32), (SEQ ID NO:34), (SEQ ID NO:36), (SEQ ID NO:38), (SEQ ID NO:40), (SEQ ID NO:42), (SEQ ID NO:46), (SEQ ID NO:48), (SEQ ID NO:50), (SEQ ID NO:52), (SEQ ID NO:54), (SEQ ID NO:56), (SEQ ID NO:58), and (SEQ ID NO:60).

NO:29), (SEQ ID NO:31), (SEQ ID NO:33), (SEQ ID NO:35), (SEQ ID NO:39), (SEQ ID NO:41), (SEQ ID NO:43), (SEQ ID NO:45), (SEQ ID NO:47), (SEQ ID NO:49), (SEQ ID NO:51), (SEQ ID NO:53), (SEQ ID NO:55), and (SEQ ID NO:59).

Vaccines may comprise coding sequences for consensus protein UL83 SEQ ID NO:20 and/or SEQ ID NO:40 and/or SEQ ID NO:6). Vaccines may comprise coding sequences for consensus protein UL83 (SEQ ID NO:20 and/or SEQ ID NO:40 and/or SEQ ID NO:60) plus one or more coding sequences for gB, gM, gN, gH, gL, gO, UL128, UL130 and UL131a. Vaccines may comprise coding sequences for consensus protein UL83 (SEQ ID NO:20 and/or SEQ ID NO:40 and/or SEQ ID NO:60) plus coding sequences for one or more of (SEQ ID NO:2), (SEQ ID NO:4), (SEQ ID NO:6), (SEQ ID NO:8), (SEQ ID NO:10), (SEQ ID NO:12), (SEQ ID NO:14), (SEQ ID NO:16), (SEQ ID NO:18), (SEQ ID NO:22), (SEQ ID NO:24), (SEQ ID NO:26), (SEQ ID NO:28), (SEQ ID NO:30), (SEQ ID NO:32), (SEQ ID NO:34), (SEQ ID NO:36), (SEQ ID NO:38), (SEQ ID NO:42), (SEQ ID NO:44), (SEQ ID NO:46), (SEQ ID NO:48), (SEQ ID NO:50), (SEQ ID NO:52), (SEQ ID NO:54), (SEQ ID NO:56), and (SEQ ID NO:58).

Vaccines may comprise specific coding sequences encoding consensus protein UL83 SEQ ID NO:19 and/or SEQ ID NO:39 and/or SEQ ID NO:59. Vaccines may comprise consensus protein UL83 a coding sequences SEQ ID NO:19 and/or SEQ ID NO:39 and/or SEQ ID NO:59 plus one or more coding sequences for gB, gM, gN, gH, gL, gO, UL128, UL130 and UL131a. Vaccines may comprise UL83 coding sequences (SEQ ID NO:19 and/or SEQ ID NO:39 and/or SEQ ID NO:59) plus consensus protein coding sequences (SEQ ID NO:1), (SEQ ID NO:3), (SEQ ID NO:5), (SEQ ID NO:7), (SEQ ID NO:9), (SEQ ID NO:11), (SEQ ID NO:13), (SEQ ID NO:15), (SEQ ID NO:17), (SEQ ID NO:21), (SEQ ID NO:23), (SEQ ID NO:25), (SEQ ID NO:27), (SEQ ID NO:29), (SEQ ID NO:31), (SEQ ID NO:33), (SEQ ID NO:35), (SEQ ID NO:37), (SEQ ID NO:41), (SEQ ID NO:43), (SEQ ID NO:45), (SEQ ID NO:47), (SEQ ID NO:49), (SEQ ID NO:51), (SEQ ID NO:53), (SEQ ID NO:55), and (SEQ ID NO:57).

Vaccines may comprise specific coding sequences encoding consensus protein HSV1-gB, HSV1-gH, HSV1-gL, HSV1-gC, or HSV1-gD, optionally with an IgE leader sequence and/or HA tag. Vaccines may comprise any one of the specific coding sequences encoding a consensus HSV1 protein, plus one or more coding sequences for any one or more of the other HSV1 consensus proteins. Vaccines may comprise a HSV1 coding sequence (DNA sequence) plus a consensus HSV1 coding sequence for any one or more of the other HSV1 coding sequences.

Vaccines may comprise specific coding sequences encoding consensus protein HSV2-gB, HSV2-gH, HSV2-gL, HSV2-gC, or HSV2-gD, optionally with an IgE leader sequence and/or HA tag. Vaccines may comprise any one of the specific coding sequences encoding a consensus HSV2 protein, plus one or more coding sequences for any one or more of the other HSV2 consensus proteins. Vaccines may comprise a HSV2 coding sequence (DNA sequence) plus a consensus HSV2 coding sequence for any one or more of the other HSV2 coding sequences.

Vaccines may comprise specific coding sequences encoding consensus protein CeHV1-gB, CeHV1-gH, CeHV1-gL, CeHV1-gC, or CeHV1-gD, optionally with an IgE leader sequence and/or HA tag. Vaccines may comprise any one of the specific coding sequences encoding a consensus CeHV1 protein, plus one or more coding sequences for any one or

more of the other CeHV1 consensus proteins. Vaccines may comprise a CeHV1 coding sequence (DNA sequence) plus a consensus CeHV1 coding sequence for any one or more of the other CeHV1 coding sequences.

Vaccines may comprise specific coding sequences encoding consensus protein VZV-gB, VZV-gH, VZV-gL, VZV-gC, VZV-gK, VZV-gM, VZV-gN, VZV-gE, or VZV-gI, optionally with an IgE leader sequence and/or HA tag. Vaccines may comprise any one of the specific coding sequences encoding a consensus VZV protein, plus one or more coding sequences for any one or more of the other VZV consensus proteins. Vaccines may comprise a VZV coding sequence (DNA sequence) plus a consensus VZV coding sequence for any one or more of the other VZV coding sequences.

Some alternative embodiments include those which comprise nucleic acid sequences encoding immunogenic fragments of one or more herpes virus antigens, one or more proteins homologous to herpes virus antigens, and immunogenic fragments of one or more proteins homologous to herpes virus antigens. Some alternative embodiments include those which comprise one or more herpes virus antigen proteins, immunogenic fragments of one or more herpes virus antigens, one or more proteins homologous to herpes virus antigens, and immunogenic fragments of one or more proteins homologous to herpes virus antigens.

Some embodiments provide methods of generating immune responses against herpes virus proteins comprise administering to an individual one or more compositions which collectively comprise one or more coding sequences or combinations described herein. Some embodiments provide methods of prophylactically vaccinating an individual against herpes virus infection comprise administering one or more compositions which collectively comprise one or more coding sequences or combinations described herein. Some embodiments provide methods of therapeutically vaccinating an individual has been infected with herpes virus comprise administering one or more compositions which collectively comprise one or more coding sequences or combinations described herein.

The vaccine may be a DNA vaccine. The DNA vaccine may comprise a plurality of the same or different plasmids comprising one or more of consensus herpes virus nucleic acid sequences. The DNA vaccine may comprise one or more nucleic acid sequences that encode one or more consensus herpes virus antigens. When the DNA vaccine comprises more than one consensus herpes virus nucleic acid sequences, all such sequences may be present on a single plasmid, or each such sequences may be present on a different plasmids, or some plasmids may comprise a single consensus herpes virus nucleic acid sequences while other plasmids have more than one consensus herpes virus nucleic acid sequences. In addition, DNA vaccines may further comprise one or more consensus coding sequences for one or more herpes virus antigens. Such additional coding sequences may be on the same or different plasmids from each other and from the plasmids comprising one or more of consensus pros

DNA vaccines are disclosed in U.S. Pat. Nos. 5,593,972, 5,739,118, 5,817,637, 5,830,876, 5,962,428, 5,981,505, 5,580,859, 5,703,055, and 5,676,594, which are incorporated herein fully by reference. The DNA vaccine can further comprise elements or reagents that inhibit it from integrating into the chromosome. The vaccine can be an RNA of the herpes virus antigen. The RNA vaccine can be introduced into the cell.

The vaccine can be a recombinant vaccine comprising the genetic construct or antigen described above. The vaccine can also comprise one or more consensus herpes virus antigen in the form of one or more protein subunits, one or more killed viral particles comprising one or more consensus herpes virus antigens, or one or more attenuated viral particles comprising one or more consensus herpes virus antigens. The attenuated vaccine can be attenuated live vaccines, killed vaccines and vaccines that use recombinant vectors to deliver foreign genes that encode one or more consensus herpes virus antigens, and well as subunit and glycoprotein vaccines. Examples of attenuated live vaccines, those using recombinant vectors to deliver foreign antigens, subunit vaccines and glycoprotein vaccines are described in U.S. Pat. Nos. 4,510,245; 4,797,368; 4,722,848; 4,790,987; 4,920,209; 5,017,487; 5,077,044; 5,110,587; 5,112,749; 5,174,993; 5,223,424; 5,225,336; 5,240,703; 5,242,829; 5,294,441; 5,294,548; 5,310,668; 5,387,744; 5,389,368; 5,424,065; 5,451,499; 5,453,364; 5,462,734; 5,470,734; 5,474,935; 5,482,713; 5,591,439; 5,643,579; 5,650,309; 5,698,202; 5,955,088; 6,034,298; 6,042,836; 6,156,319 and 6,589,529, which are each incorporated herein by reference.

The vaccine can comprise vectors and/or proteins directed to herpes virus serotypes from particular regions in the world. The vaccine can also be directed against herpes virus serotypes from multiple regions in the world.

The vaccine provided may be used to induce immune responses including therapeutic or prophylactic immune responses. Antibodies and/or killer T cells may be generated which are directed to the consensus herpes virus antigen, and also broadly across multiple subtypes of herpes viruses. Such antibodies and cells may be isolated.

The vaccine can further comprise a pharmaceutically acceptable excipient. The pharmaceutically acceptable excipient can be functional molecules as vehicles, adjuvants, carriers, or diluents. The pharmaceutically acceptable excipient can be a transfection facilitating agent, which can include surface active agents, such as immune-stimulating complexes (ISCOMS), Freund's incomplete adjuvant, LPS analog including monophosphoryl lipid A, muramyl peptides, quinone analogs, vesicles such as squalene and squalene, hyaluronic acid, lipids, liposomes, calcium ions, viral proteins, polyanions, polycations, or nanoparticles, or other known transfection facilitating agents.

The transfection facilitating agent is a polyanion, polycation, including poly-L-glutamate (LGS), or lipid. The transfection facilitating agent is poly-L-glutamate, and more preferably, the poly-L-glutamate is present in the vaccine at a concentration less than 6 mg/ml. The transfection facilitating agent can also include surface active agents such as immune-stimulating complexes (ISCOMS), Freund's incomplete adjuvant, LPS analog including monophosphoryl lipid A, muramyl peptides, quinone analogs and vesicles such as squalene and squalene, and hyaluronic acid can also be used administered in conjunction with the genetic construct. In some embodiments, the DNA vector vaccines can also include a transfection facilitating agent such as lipids, liposomes, including lecithin liposomes or other liposomes known in the art, as a DNA-liposome mixture (see for example WO9324640), calcium ions, viral proteins, polyanions, polycations, or nanoparticles, or other known transfection facilitating agents. Preferably, the transfection facilitating agent is a polyanion, polycation, including poly-L-glutamate (LGS), or lipid. Concentration of the transfection agent in the vaccine is less than 4 mg/ml, less than 2 mg/ml, less than 1 mg/ml, less than 0.750 mg/ml, less than 0.500

mg/ml, less than 0.250 mg/ml, less than 0.100 mg/ml, less than 0.050 mg/ml, or less than 0.010 mg/ml.

The pharmaceutically acceptable excipient may be an adjuvant. The adjuvant may be other genes that are expressed in alternative plasmid or are delivered as proteins in combination with the plasmid above in the vaccine. The adjuvant may be selected from the group consisting of: α -interferon (IFN- α), β -interferon (IFN- β), γ -interferon, platelet derived growth factor (PDGF), TNF α , TNF β , GM-CSF, epidermal growth factor (EGF), cutaneous T cell-attracting chemokine (CTACK), epithelial thymus-expressed chemokine (TECK), mucosae-associated epithelial chemokine (MEC), IL-12, IL-15, MHC, CD80, CD86 including IL-15 having the signal sequence deleted and optionally including the signal peptide from IgE. The adjuvant may be IL-12, IL-15, IL-28, CTACK, TECK, platelet derived growth factor (PDGF), TNF α , TNF β , GM-CSF, epidermal growth factor (EGF), IL-1, IL-2, IL-4, IL-5, IL-6, IL-10, IL-12, IL-18, or a combination thereof.

Other genes which may be useful adjuvants include those encoding: MCP-1, MIP-1a, MIP-1p, IL-8, RANTES, L-selectin, P-selectin, E-selectin, CD34, GlyCAM-1, MadCAM-1, LFA-1, VLA-1, Mac-1, p150.95, PECAM, TCAM-1, TCAM-2, TCAM-3, CD2, LFA-3, M-CSF, G-CSF, IL-4, mutant forms of IL-18, CD40, CD40L, vascular growth factor, fibroblast growth factor, IL-7, nerve growth factor, vascular endothelial growth factor, Fas, TNF receptor, Flt, Apo-1, p55, WSL-1, DR3, TRAMP, Apo-3, AIR, LARD, NGRF, DR4, DR5, KILLER, TRAIL-R2, TRICK2, DR6, Caspase ICE, Fos, c-jun, Sp-1, Ap-1, Ap-2, p38, p65Rel, MyD88, TRAK, TRAF6, Tkb, Inactive NTK, SAP K, SAP-1, INK, interferon response genes, NFkB, Bax, TRAIL, TRAILrec, TRAILrecDRC5, TRAIL-R3, TRAIL-R4, RANK, RANK LIGAND, Ox40, Ox40 LIGAND, NKG2D, MICA, MICB, NKG2A, NKG2B, NKG2C, NKG2E, NKG2F, TAP1, TAP2 and functional fragments thereof.

The vaccine can further comprise a genetic vaccine facilitator agent as described in U.S. Pat. No. 5,739,118, filed Apr. 1, 1994, which is fully incorporated by reference.

5. Methods of Delivery

Provided herein is a method for delivering the pharmaceutical formulations, preferably vaccines, for providing genetic constructs and proteins of the herpes virus antigen which comprise epitopes that make them particular effective immunogens against which an immune response to herpes virus viral infections can be induced. The method of delivering the vaccine, or vaccination, can be provided to induce a therapeutic and/or prophylactic immune response. The vaccination process can generate in the mammal an immune response against a plurality of herpes virus subtypes. The vaccine can be delivered to an individual to modulate the activity of the mammal's immune system and enhance the immune response. The delivery of the vaccine can be the transfection of the HA antigen as a nucleic acid molecule that is expressed in the cell and delivered to the surface of the cell upon which the immune system recognized and induces a cellular, humoral, or cellular and humoral response. The delivery of the vaccine can be used to induce or elicit and immune response in mammals against a plurality of herpes viruses, herpes family specific, by administering to the mammals the relevant herpes virus family vaccine as discussed herein.

Upon delivery of the vaccine to the mammal, and thereupon the vector into the cells of the mammal, the transfected cells will express and secrete the corresponding one or more herpes virusantigens. These secreted proteins, or synthetic antigens, will be recognized as foreign by the immune system, which will mount an immune response that can include: antibodies made against the antigens, and T-cell response specifically against the antigen. In some examples, a mammal vaccinated with the vaccines discussed herein will have a primed immune system and when challenged with a relevant herpes viral strain, the primed immune system will allow for rapid clearing of subsequent herpes viruses, whether through the humoral, cellular, or both. The vaccine can be delivered to an individual to modulate the activity of the individual's immune system thereby enhancing the immune response.

The vaccine can be delivered in the form of a DNA vaccine and methods of delivering a DNA vaccines are described in U.S. Pat. Nos. 4,945,050 and 5,036,006, which are both incorporated fully by reference.

The vaccine can be administered to a mammal to elicit an immune response in a mammal. The mammal can be human, non-human primate, cow, pig, sheep, goat, antelope, bison, water buffalo, bovids, deer, hedgehogs, elephants, llama, alpaca, mice, rats, or chicken, and preferably human, cow, pig, or chicken.

a. Combination Treatments

The pharmaceutical compositions, preferably vaccines, can be administered in combination with one or more herpes virus antigens. The vaccine can be administered in combination with proteins or genes encoding adjuvants, which can include: α -interferon (IFN- α), β -interferon (IFN- β), γ -interferon, IL-12, IL-15, IL-28, CTACK, TECK, platelet derived growth factor (PDGF), TNF α , TNF β , GM-CSF, epidermal growth factor (EGF), IL-1, IL-2, IL-4, IL-5, IL-6, IL-10, IL-12, IL-18, MCP-1, MIP-1a, MIP-1p, IL-8, RANTES, L-selectin, P-selectin, E-selectin, CD34, GlyCAM-1, MadCAM-1, LFA-1, VLA-1, Mac-1, p150.95, PECAM, ICAM-1, ICAM-2, ICAM-3, CD2, LFA-3, M-CSF, G-CSF, IL-4, mutant forms of IL-18, CD40, CD40L, vascular growth factor, fibroblast growth factor, IL-7, nerve growth factor, vascular endothelial growth factor, Fas, TNF receptor, Flt, Apo-1, p55, WSL-1, DR3, TRAMP, Apo-3, AIR, LARD, NGRF, DR4, DR5, KILLER, TRAIL-R2, TRICK2, DR6, Caspase ICE, Fos, c-jun, Sp-1, Ap-1, Ap-2, p38, p65Rel, MyD88, IRAK, TRAF6, I κ B, Inactive NIK, SAP K, SAP-1, JNK, interferon response genes, NF κ B, Bax, TRAIL, TRAILrec, TRAILrecDRC5, TRAIL-R3, TRAIL-R4, RANK, RANK LIGAND, Ox40, Ox40 LIGAND, NKG2D, MICA, MICB, NKG2A, NKG2B, NKG2C, NKG2E, NKG2F, TAP1, or TAP2, or functional fragments thereof.

b. Routes of Administration

The vaccine can be administered by different routes including orally, parenterally, sublingually, transdermally, rectally, transmucosally, topically, via inhalation, via buccal administration, intrapleurally, intravenous, intraarterial, intraperitoneal, subcutaneous, intramuscular, intranasal intrathecal, and intraarticular or combinations thereof. For veterinary use, the composition can be administered as a suitably acceptable formulation in accordance with normal veterinary practice. The veterinarian can readily determine the dosing regimen and route of administration that is most appropriate for a particular animal. The vaccine can be administered by traditional syringes, needleless injection devices, "microprojectile bombardment gone guns", or other physical methods such as electroporation ("EP"), "hydrodynamic method", or ultrasound.

The vector of the vaccine can be delivered to the mammal by several well known technologies including DNA injection (also referred to as DNA vaccination) with and without in vivo electroporation, liposome mediated, nanoparticle facilitated, recombinant vectors such as recombinant adenovirus, recombinant adenovirus associated virus and recombinant vaccinia. The herpes virus antigen can be delivered via DNA injection and along with in vivo electroporation.

c. Electroporation

Administration of the vaccine via electroporation of the plasmids of the vaccine may be accomplished using electroporation devices that can be configured to deliver to a desired tissue of a mammal a pulse of energy effective to cause reversible pores to form in cell membranes, and preferable the pulse of energy is a constant current similar to a preset current input by a user. The electroporation device may comprise an electroporation component and an electrode assembly or handle assembly. The electroporation component may include and incorporate one or more of the various elements of the electroporation devices, including: controller, current waveform generator, impedance tester, waveform logger, input element, status reporting element, communication port, memory component, power source, and power switch. The electroporation may be accomplished using an in vivo electroporation device, for example CELLECTRA® EP system (Inovio Pharmaceuticals, Inc., Blue Bell, Pa.) or Elgen electroporator (Inovio Pharmaceuticals, Inc., Blue Bell, Pa.) to facilitate transfection of cells by the plasmid.

The electroporation component may function as one element of the electroporation devices, and the other elements are separate elements (or components) in communication with the electroporation component. The electroporation component may function as more than one element of the electroporation devices, which may be in communication with still other elements of the electroporation devices separate from the electroporation component. The elements of the electroporation devices existing as parts of one electromechanical or mechanical device may not be limited as the elements can function as one device or as separate elements in communication with one another. The electroporation component may be capable of delivering the pulse of energy that produces the constant current in the desired tissue, and includes a feedback mechanism. The electrode assembly may include an electrode array having a plurality of electrodes in a spatial arrangement, wherein the electrode assembly receives the pulse of energy from the electroporation component and delivers same to the desired tissue through the electrodes. At least one of the plurality of electrodes is neutral during delivery of the pulse of energy and measures impedance in the desired tissue and communicates the impedance to the electroporation component. The feedback mechanism may receive the measured impedance and can adjust the pulse of energy delivered by the electroporation component to maintain the constant current.

A plurality of electrodes may deliver the pulse of energy in a decentralized pattern. The plurality of electrodes may deliver the pulse of energy in the decentralized pattern through the control of the electrodes under a programmed sequence, and the programmed sequence is input by a user to the electroporation component. The programmed sequence may comprise a plurality of pulses delivered in sequence, wherein each pulse of the plurality of pulses is delivered by at least two active electrodes with one neutral electrode that measures impedance, and wherein a subsequent pulse of the plurality of pulses is delivered by a

different one of at least two active electrodes with one neutral electrode that measures impedance.

The feedback mechanism may be performed by either hardware or software. The feedback mechanism may be performed by an analog closed-loop circuit. The feedback occurs every 50 μ s, 20 μ s, 10 μ s or 1 μ s, but is preferably a real-time feedback or instantaneous (i.e., substantially instantaneous as determined by available techniques for determining response time). The neutral electrode may measure the impedance in the desired tissue and communicates the impedance to the feedback mechanism, and the feedback mechanism responds to the impedance and adjusts the pulse of energy to maintain the constant current at a value similar to the preset current. The feedback mechanism may maintain the constant current continuously and instantaneously during the delivery of the pulse of energy.

Examples of electroporation devices and electroporation methods that may facilitate delivery of the DNA vaccines of the present invention, include those described in U.S. Pat. No. 7,245,963 by Draghia-Akli, et al., U.S. Patent Pub. 2005/0052630 submitted by Smith, et al., the contents of which are hereby incorporated by reference in their entirety. Other electroporation devices and electroporation methods that may be used for facilitating delivery of the DNA vaccines include those provided in co-pending and co-owned U.S. patent application Ser. No. 11/874,072, filed Oct. 17, 2007, which claims the benefit under 35 USC 119(e) to U.S. Provisional Application Ser. No. 60/852,149, filed Oct. 17, 2006, and 60/978,982, filed Oct. 10, 2007, all of which are hereby incorporated in their entirety.

U.S. Pat. No. 7,245,963 by Draghia-Akli, et al. describes modular electrode systems and their use for facilitating the introduction of a biomolecule into cells of a selected tissue in a body or plant. The modular electrode systems may comprise a plurality of needle electrodes; a hypodermic needle; an electrical connector that provides a conductive link from a programmable constant-current pulse controller to the plurality of needle electrodes; and a power source. An operator can grasp the plurality of needle electrodes that are mounted on a support structure and firmly insert them into the selected tissue in a body or plant. The biomolecules are then delivered via the hypodermic needle into the selected tissue. The programmable constant-current pulse controller is activated and constant-current electrical pulse is applied to the plurality of needle electrodes. The applied constant-current electrical pulse facilitates the introduction of the biomolecule into the cell between the plurality of electrodes. The entire content of U.S. Pat. No. 7,245,963 is hereby incorporated by reference.

U.S. Patent Pub. 2005/0052630 submitted by Smith, et al. describes an electroporation device which may be used to effectively facilitate the introduction of a biomolecule into cells of a selected tissue in a body or plant. The electroporation device comprises an electro-kinetic device ("EKD device") whose operation is specified by software or firmware. The EKD device produces a series of programmable constant-current pulse patterns between electrodes in an array based on user control and input of the pulse parameters, and allows the storage and acquisition of current waveform data. The electroporation device also comprises a replaceable electrode disk having an array of needle electrodes, a central injection channel for an injection needle, and a removable guide disk. The entire content of U.S. Patent Pub. 2005/0052630 is hereby incorporated by reference.

The electrode arrays and methods described in U.S. Pat. No. 7,245,963 and U.S. Patent Pub. 2005/0052630 may be

adapted for deep penetration into not only tissues such as muscle, but also other tissues or organs. Because of the configuration of the electrode array, the injection needle (to deliver the biomolecule of choice) is also inserted completely into the target organ, and the injection is administered perpendicular to the target issue, in the area that is pre-delineated by the electrodes. The electrodes described in U.S. Pat. No. 7,245,963 and U.S. Patent Pub. 2005/005263 are preferably 20 mm long and 21 gauge.

Additionally, contemplated in some embodiments that incorporate electroporation devices and uses thereof, there are electroporation devices that are those described in the following patents: U.S. Pat. No. 5,273,525 issued Dec. 28, 1993, U.S. Pat. No. 6,110,161 issued Aug. 29, 2000, U.S. Pat. No. 6,261,281 issued Jul. 17, 2001, and U.S. Pat. No. 6,958,060 issued Oct. 25, 2005, and U.S. Pat. No. 6,939,862 issued Sep. 6, 2005. Furthermore, patents covering subject matter provided in U.S. Pat. No. 6,697,669 issued Feb. 24, 2004, which concerns delivery of DNA using any of a variety of devices, and U.S. Pat. No. 7,328,064 issued Feb. 5, 2008, drawn to method of injecting DNA are contemplated herein. The above-patents are incorporated by reference in their entirety.

d. Method of Preparing Vaccine

Provided herein is methods for preparing the DNA plasmids that comprise the DNA vaccines discussed herein. The DNA plasmids, after the final subcloning step into the mammalian expression plasmid, can be used to inoculate a cell culture in a large scale fermentation tank, using known methods in the art.

The DNA plasmids for use with the EP devices of the present invention can be formulated or manufactured using a combination of known devices and techniques, but preferably they are manufactured using an optimized plasmid manufacturing technique that is described in a licensed, co-pending U.S. provisional application U.S. Ser. No. 60/939,792, which was filed on May 23, 2007. In some examples, the DNA plasmids used in these studies can be formulated at concentrations greater than or equal to 10 mg/mL. The manufacturing techniques also include or incorporate various devices and protocols that are commonly known to those of ordinary skill in the art, in addition to those described in U.S. Ser. No. 60/939,792, including those described in a licensed patent, U.S. Pat. No. 7,238,522, which issued on Jul. 3, 2007. The above-referenced application and patent, U.S. Ser. No. 60/939,792 and U.S. Pat. No. 7,238,522, respectively, are hereby incorporated in their entirety.

EXAMPLES

The present invention is further illustrated in the following Examples. It should be understood that these Examples, while indicating preferred embodiments of the invention, are given by way of illustration only. From the above discussion and these Examples, one skilled in the art can ascertain the essential characteristics of this invention, and without departing from the spirit and scope thereof, can make various changes and modifications of the invention to adapt it to various usages and conditions. Thus, various modifications of the invention in addition to those shown and described herein will be apparent to those skilled in the art from the foregoing description. Such modifications are also intended to fall within the scope of the appended claims.

Example 1 Generating Herpes Antigens and Expression Constructs

A DNA vaccine strategy was employed that focused on glycoproteins, chaperone proteins and matrix proteins of

herpes virus family. To increase the potential breadth of immunity elicited by each viral antigen (Ag), phylogenetic diversity was first examined to assess polymorphism and to aid in the production of clinically-relevant consensus amino acid sequences.

Genetic and Statistical Analysis

Phylogenetic and molecular evolutionary analyses were conducted using MEGA version 5 (Tamura, Peterson, Stecher, Nei, and Kumar 2011) to estimate diversity among clinically relevant and publically available herpes target protein sequences used for generating consensus vaccine Ags. Neighbor-joining phylogenetic reconstruction analysis using the bootstrap method with 1,000 bootstrap replications was used to generate bootstrap consensus trees with radiation view. P-distances are shown for HCMV, for example (FIG. 17).

All values are reported as the mean \pm SEM. Analysis between groups was completed by ANOVA with a post-hoc Dunnett's test to correct for multiple comparisons to one control (HCMV infected). All statistical analysis was carried out using GraphPad Prism (GraphPad Software Inc., La Jolla, Calif.) or the Statistical Package for the Social Sciences (SPSS, Chicago, Ill.).

Strategies for generating the consensus amino acid sequences for each herpes immunogen are outlined, below. In general, consensus sequences from highly conserved herpes proteins were used for vaccine immunogens while consensus sequences from specific, clinically relevant subgroups were used for the highly divergent proteins.

Amino acid sequences of herpes vaccine proteins were generated by taking the consensus of publically available (GenBank) and clinically relevant strains (passaged no more than six times in tissue culture) using Vector NTI software (Invitrogen) for sequence alignment. Some plasmids (VZV gHgL, VZV gEgI, VZV gMgN, HSV1 gHgL, HSV1 gCgD, HSV2 gHgL, HSV2 gCgD, CeHV1 gHgL, CeHV1 gCgD, pCMV-gHgL, pCMV-gMgN, and pCMV-UL) expressed multiple herpes proteins which were separated by a cleavage site (furin site SEQ ID NO:63) for the co-expression of structurally-relevant macromolecules. Genetic optimization of DNA vaccines included codon and RNA optimization for protein expression in humans and all genes were synthesized and subcloned into a modified pVAX1 mammalian expression vector (GeneArt, Regensburg, Germany or GenScript, Piscataway, N.J.).

HCMV Specific Analysis

Phylogenetic analysis of the HCMV gB confirmed the presence of four main variants (gB1-gB4) and one nonprototypic variant (gB5) (FIG. 17a). Since the gB protein is relatively conserved among clinical and low-passage strains (~86% identical), we chose the consensus of these sequences to represent our DNA vaccine-encoded Ag. The vaccine sequence was phylogenetically closest to the gB1 genotype which has been found in some cases to account for the majority of highly symptomatic individuals in the clinic.

Next, components of the HCMV gCIII fusion complex, gH, gL and gO were developed as candidate immunogens for evaluation as a DNA vaccine. Phylogenetic analysis of gH confirmed the presence of two main genotypes in addition to a possible third group including the newly reported JHC strain that was isolated from a bone marrow transplant patient [Jung, et. Al., *Virus Res.* 2011 June; 158(1-2):298] (FIG. 17b). Analysis confirmed a low level of amino acid variation among the gHs (~7%) which may explain why anti-gH MAbs appear broadly reactive. Due to this high level of conservation, the DNA vaccine consensus immunogen fell right between gH1 and gH2 and was closest to the

putative third gH group along with the JHC clinical isolate. Phylogenetic analysis of the gL protein, while similarly highly conserved (~91%), was less distinctly grouped (FIG. 17c). Upon removal of amino acid sequences of gLs from strains extensively passaged the resultant DNA consensus immunogen fell closest on the tree to the JHC and Merlin clinical isolates and farthest away from the AD169 and Towne lab-adapted strains. The third component of the classically defined gCIII complex is the gO, which is highly glycosylated, and is highly variable at the 5' end. Since gO polymorphism was high (~55%), we chose the consensus sequence of the gO5 genotype group for our target immunogen since this group has been previously described to be genetically linked with the gN-4c genotype, the largest gN-4 variant group and most seroprevalent (FIG. 17f). Identity within the gO5 subgroup was ~99% and thus, the consensus Ag was phylogenetically grouped with this subgroup that also included the Merlin and JP clinical isolates.

Novel candidate vaccine immunogens HCMV gM and gN heterodimerize in the ER by both covalent disulfide bonding and noncovalent interaction to form the viral infectivity complex. While the gM is highly conserved among the CMV (~95%), the gN is variable (~45). Due to this relatively high identity among the gM, consensus of all clinically relevant sequences determined our candidate vaccine immunogen (FIG. 17d). Conversely, due to the highly modified nature of gN, characterized by almost exclusive O-linked sugars, consensus of the gN-4 subtype was used as vaccine immunogen since this subgroup was reported to be the most prevalent of all clinical isolates in North America, Europe, China, and Australia (FIG. 17e). Thus, this sequence was phylogenetically closest to the gN4b subtype, which occurs directly between the gN4a and gN4c groups, all of which constitute the gN4 group.

Recently, it has been shown that UL128, UL130, and UL131A can form a pentameric complex with gH and gL, instead of the classically defined association of gH/gL/gO for the gCIII fusion complex. Furthermore, that this complex has been described to elicit potent mAbs. Due to the relatively high level of amino acid conservation upon removal of high-passaged and lab-adapted strains (~87% for UL128, ~86% for UL130, and ~73% for UL131A), consensus sequences were used for each gene for candidate vaccine immunogens (FIG. 17g-i). The UL128 vaccine sequence was phylogenetically grouped in a group including the Merlin and Davis isolates, as well as the Ad169 strain. However, Both of the UL130 and UL131A sequences were phylogenetically distant from the Towne and AD169 lab strains, respectively, which have lost their ability to infect endothelial cells, epithelial cells, and leukocytes due to deletions or mutations of these genes. And lastly, the UL83 protein (pp65) was chosen due to its current use in recent vaccine strategies as a T cell target. This protein was initially attractive based upon its apparent dominance in the cellular immune response to HCMV since it was recognized by the majority of virus-specific CD8 T cells. This protein is highly conserved among the CMV and was ~97% identical when no accounting for the 3' truncation associated with many published sequences (FIG. 17j). Thus, consensus of the UL83 proteins was used for the target vaccine Ag and was phylogenetically similar to the JP, VR1814, Merlin and Ad169 strains, but further from the Towne, Toledo, and JHC strains.

Full-length candidate CMV immunogens were next used to construct plasmid DNA vaccines. Each Ag was genetically optimized for expression in humans, commercially synthesized, and then subcloned into a modified pVAX1

mammalian expression vector. In addition, proteins requiring heterologous interaction for the construction of functional virion surface complexes were encoded in combination within the same DNA vaccine plasmid. Multiple protein-expressing plasmids gHgL, gMgN, and pUL encoded ubiquitous endo-proteolytic furin cleavage sites between immunogens to facilitate post-translational cleavage and modification. In this way, co-expression of structurally and functionally relevant proteins hypothetically facilitates the formation of macromolecular complexes that may better express clinically- and virologically-relevant B cell epitopic determinants. This may be particularly critical in cases where coexpression is required for productive expression; gH requires coexpression of gL for intracellular transport and terminal carbohydrate modifications [Spaete, 1993 #1195] and similarly, gL remains localized in the ER when expressed in the absence of gH.

One plasmid included coding sequences for HCMV-gB, a 907-9 amino acid protein which forms a homodimer and is a type I membrane protein. Another plasmid included coding sequences for HCMV-gM, a 373 amino acid protein linked to coding sequences for HCMV-gN, a 139 amino acid protein. The HCMV-gM and gN proteins form a heterodimer and are involved in infectivity. Another plasmid included coding sequences for HCMV-gH, a 740 amino acid protein linked to coding sequences for gL, a 278 amino acid protein. The HCMV-gH protein and the HCMV-gL protein form a heterotrimer with the HCMV-gO-gCIII complex involved in viral fusion. The HCMV-gH and gL proteins can also form a disulfide-linked heterodimer in the ER. Another plasmid included coding sequences for HCMV-gO, a 472 amino acid protein that forms the aforementioned heterotrimer with the HCMV-gH and gL. Another plasmid encodes coding sequences for HCMV-pUL (UL128), a 140 amino acid protein, linked to coding sequences for HCMV-UL130, a 215 amino acid protein linked to coding sequences for HCMV-UL131A, a 77 amino acid protein. These three proteins serve as chaperones for HCMV-gO. Another plasmid encodes HCMV-gUL83 (pp65); which is a T cell target protein.

In one embodiment, ten coding sequences (SEQ TD NO:1, SEQ TD NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17 and SEQ ID NO:19) for HCMV consensus amino acid sequences (SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18 and SEQ ID NO:20) were included on six separate expression vector plasmids. Single gene constructs were provided for gB (plasmid 1), (plasmid 4) gO and gUL83 (modified plasmid 6). Chimeric genes encoding fusion proteins were provided for constructs encoding gM and gN (plasmid 2), gH and gL (plasmid 3), and UL128, UL130 and UL131a (plasmid 5) which are expressed as a single polyprotein. In each instance of a fusion protein, the coding sequences for the different antigens in the polyprotein were linked sequences encoding the furin proteolytic cleavage site (SEQ ID NO:63). The coding sequences for the fusion proteins also included coding sequence for the IgE signal peptide (SEQ ID NO:61) at the N terminal of the polyprotein as well as coding sequences for an HA Tag (SEQ TD NO:62) which is linked at the C terminal of each HCMV antigen in the polyprotein. Following processing at the proteolytic cleavage site(s) of the polyprotein into separate proteins, each protein comprises an HA Tag. The coding sequences for the single antigen constructs each were provided with coding sequences for the IgE signal peptide (SEQ ID NO:61) to be

included at the N terminal of each translation product. Coding sequences for gB and gO were each also provided with coding sequences for an HA Tag (SEQ ID NO:62) so that the C terminal of each HCMV antigen protein comprises an HA Tag. Coding sequences for gUL83 in modified plasmid 6 do not contain coding sequences for HA Tags. However, another version of modified plasmid 6 can be constructed to contain coding sequences for an HA Tag (SEQ ID NO:62) so that the C terminal of the HCMV antigen protein comprises an HA Tag.

Each of plasmids 1-6 and modified plasmids 1-6 may be made using the variant pVax1 (FIG. 1, SEQ ID NO:76) disclosed herein.

Plasmid 1 (FIG. 2) is the variant pVax1 with an insert having regulatory elements operably linked to SEQ IN NO:41, i.e. nucleic acid sequence that encodes IgE leader linked to consensus gB linked to the HA Tag, thus encoding the protein SEQ ID NO:42.

Plasmid 2 (FIG. 3) is a variant pVax1 with an insert having regulatory elements operably linked to nucleic acid sequence SEQ ID NO:64 that encodes IgE leader linked to consensus gM linked to the HA tag linked to a furin proteolytic cleavage site linked to nucleic acid sequence that consensus gN4-c linked to an HA Tag, thus encoding the fusion protein SEQ ID NO:65.

Plasmid 3 (FIG. 4) is a variant pVax1 with an insert having regulatory elements operably linked to nucleic acid sequence SEQ ID NO:66 that encodes IgE leader linked to consensus gH linked to the HA tag linked to a furin proteolytic cleavage site linked to nucleic acid sequence that consensus gL linked to an HA Tag, thus encoding the fusion protein SEQ ID NO:67.

Plasmid 4 (FIG. 5) is a variant pVax1 with an insert having regulatory elements operably linked to nucleic acid sequence SEQ ID NO:51 that encodes IgE leader linked to consensus gO-5 linked to and HA tag, thus encoding the protein SEQ ID NO:52.

Plasmid 5 (FIG. 6) is a variant pVax1 with an insert having regulatory elements operably linked to nucleic acid sequence SEQ ID NO:68 that encodes IgE leader linked to consensus UL131a linked to an HA Tag linked to a furin proteolytic cleavage site linked to consensus UL130 linked to an HA Tag linked to a furin proteolytic cleavage site linked to consensus UL128 linked to an HA Tag, thus encoding the fusion protein SEQ ID NO:69.

Modified plasmid 6 (FIG. 9) is a variant pVax1 with an insert having regulatory elements operably linked to SEQ ID NO:39; i.e. nucleic acid sequence that encodes IgE leader linked to consensus UL-83 (pp65), thus encoding the protein SEQ ID NO:40.

Plasmid 6 (FIG. 7) may be used in place of modified plasmid 6 if HA Tags linked to the U83 translation product is desirable. Plasmid 6 may be a variant pVax1 with an insert having regulatory elements operably linked to SEQ ID NO:59; i.e. nucleic acid sequence that encodes IgE leader linked to consensus UL-83 (pp65), thus encoding the protein SEQ ID NO:60.

In some embodiments, plasmids 1-5 may be modified so that the coding sequences for HA Tags are absent.

Modified plasmid 1 (FIG. 7) may be a variant pVax1 described herein with an insert having regulatory elements operably linked to SEQ IN NO:21, i.e. nucleic acid sequence that encodes IgE leader linked to consensus gB, thus encoding the protein SEQ ID NO:22.

Modified plasmid 2 may be a variant pVax1 described herein with an insert having regulatory elements operably linked to nucleic acid sequence SEQ ID NO:70 that encodes

IgE leader linked to consensus gM linked to a furin proteolytic cleavage site linked to nucleic acid sequence that encodes consensus gN4-c, thus encoding the fusion protein SEQ ID NO:71.

Modified plasmid 3 (FIG. 8) may be a variant pVax1 described herein with an insert having regulatory elements operably linked to nucleic acid sequence SEQ ID NO:72 that encodes IgE leader linked to consensus gH linked to a furin proteolytic cleavage site linked to nucleic acid sequence that encodes consensus gL, thus encoding the fusion protein SEQ ID NO:73.

Modified plasmid 4 may be a variant pVax1 described herein with an insert having regulatory elements operably linked to nucleic acid sequence SEQ ID NO:31 that encodes IgE leader linked to consensus gO-5 linked to, thus encoding the protein SEQ ID NO:32.

Modified plasmid 5 may be a variant pVax1 described herein with an insert having regulatory elements operably linked to nucleic acid sequence SEQ ID NO:74 that encodes IgE leader linked to consensus UL131a linked to a furin proteolytic cleavage site linked to consensus UL130 linked to a furin proteolytic cleavage site linked to consensus UL128, thus encoding the fusion protein SEQ TD NO:75.

In some embodiments, a composition comprising these six plasmids is an example of an anti-HCMV vaccine. In some embodiments of an anti-HCMV vaccine, two or more compositions which collectively comprise these six plasmids. Some embodiments provide methods of generating immune responses against HCMV proteins comprise administering to an individual one or more compositions which collectively comprise each of these six plasmids. Some embodiments provide methods of prophylactically vaccinating an individual against HCMV infection comprise administering one or more compositions which collectively comprise each of these six plasmids. Some embodiments provide methods of therapeutically vaccinating an individual has been infected with HCMV comprise administering one or more compositions which collectively comprise each of these six plasmids.

Analysis of other Herpes Viruses:

Similar to HCMV, above, similar strategy was used to identify antigens for HSV1, HSV2, CeHV1, and VZV.

For the herpes viruses from families VZV, CeHV1, HSV1, and HSV2, the following antigens were considered, based on similar criteria used for CMV, above, and consensus antigens were made and cloned into similar vectors as CMV: surface antigens envelope gB, gH, gL, gM, gN, gO, gE, gI, and gK were considered.

Plasmids were constructed for optimizing nascent coexpression of relevant proteins. In total, 21 plasmids were constructed that express HCMV gB, gM/gN, gH/gL, gO, UL128-131, and U183; VZV gHgL, gEgI, gMgN, gB, gC, and gK; HSV1 gB, gHgL, gCgD; HSV2 gB, gHgL, gCgD; and CeHV1 gB, gHgL, and gCgD, in highly-optimized DNA vaccines plasmids were constructed for optimizing nascent coexpression of relevant proteins. In total, 21 plasmids were constructed that express HCMV gB, gM/gN, gH/gL, gO, UL128-131, and U183; VZV gHgL, gEgI, gMgN, gB, gC, and gK; HSV1 gB, gHgL, gCgD; HSV2 gB, gHgL, gCgD; and CeHV1 gB, gHgL, and gCgD in highly-optimized DNA vaccines.

Plasmids 7-21 correspond to each one of the following VZV gHgL, gEgI, gMgN, gB, gC, and gK; HSV1 gB, gHgL, gCgD; HSV2 gB, gHgL, gCgD; and CeHV1 gB, gHgL, and gCgD encoding sequences cloned into variant pVax1 (FIG. 1, SEQ TD NO:76) vector disclosed herein. In some embodiments, the pVax1 has an insert having regulatory

elements operably linked to the encoding nucleic acid sequence for the herpes antigen which includes an encoding sequence for IgE leader (encoding amino acid sequence SEQ ID NO:61) linked to the antigen. In some embodiments, plasmids 7-21 may be modified so that the coding sequences for HA Tags (encoding amino acid sequence SEQ ID NO:62) are linked to the N-terminal end of the antigen.

Example 2

In some embodiments, a composition comprising coding sequences for each of: HCMV: gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83, or multiple compositions which collectively comprise coding sequences for each of: gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83 are administered. The composition which comprises coding sequences of each of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83, or combinations of compositions that collectively comprise coding sequences of each of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a. In some embodiments, vaccines comprise one or more of the coding sequences encoding each of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a that have sequences selected from the group consisting of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 and 60. In some embodiments, one or more of the coding sequences is selected from the group consisting of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 and 59. In some embodiments, one or more of the coding sequences in a vaccine is selected from the group consisting of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 and 59. In some embodiments, a vaccine comprises each of the coding sequences SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17 and 19. In some embodiments, a vaccine comprises each of the coding sequences in SEQ ID NO:21, 23, 25, 27, 29, 31, 33, 35, 37 and 39. In some embodiments, a vaccine comprises each of the coding sequences in SEQ ID NO:41, 43, 45, 47, 49, 51, 53, 55, 57 and 59.

Example 3

In some embodiments, a composition comprising coding sequences for nine of: gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83, or multiple compositions which collectively comprise coding sequences for nine of: gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83 are administered. The composition may comprises coding sequences of nine of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83, or combinations of compositions that collectively comprise coding sequences of nine of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83. The following combinations 9-1 to 9-10 may be present in such vaccines: 9-1 gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a; 9-2 gB, gM, gN, gH, gL, gO, UL128, UL130, UL83; 9-3 gB, gM, gN, gH, gL, gO, UL128, UL131a, UL83; 9-4 gB, gM, gN, gH, gL, gO, UL130, UL131a, UL83; 9-5 gB, gM, gN, gH, gL, UL128, UL130, UL131a, UL83; 9-6 gB, gM, gN, gH, gO, UL128, UL130, UL131a, UL83; 9-7 gB, gM, gN, gL, gO, UL128, UL130, UL131a, UL83; 9-8 gB, gM, gH, gL, gO, UL128, UL130, UL131a, UL83; 9-9 gB, gN, gH, gL, gO, UL128, UL130, UL131a, UL83; and 9-10 gM, gN, gH, gL, gO, UL128, UL130, UL131a, UL83. In some embodiments, these vaccines comprise one or more of the coding sequences encoding each of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a that have sequences selected from

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the group consisting of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 and 60. In some embodiments, one or more of the coding sequences is selected from the group consisting of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 and 59. In some embodiments, one or more of the coding sequences in a vaccine is selected from the group consisting of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 and 59.

Example 4

In some embodiments, a composition comprising coding sequences for eight of: gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83, or multiple compositions which collectively comprise coding sequences for eight of: gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83 are administered. The composition may comprises coding sequences of eight of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83, or combinations of compositions that collectively comprise coding sequences of eight of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83. The following combinations 8-1 to 8-45 may be present in an eight antigen vaccine: 8-1: gB, gM, gN, gH, gL, gO, UL128, UL130; 8-2: gB, gM, gN, gH, gL, gO, UL128, UL131a; 8-3: gB, gM, gN, gH, gL, gO, UL128, UL83; 8-4: gB, gM, gN, gH, gL, gO, UL130, UL131a; 8-5: gB, gM, gN, gH, gL, gO, UL130, UL83; 8-6: gB, gM, gN, gH, gL, gO, UL131a, UL83; 8-7: gB, gM, gN, gH, gL, UL128, UL130, UL131a; 8-8: gB, gM, gN, gH, gL, UL128, UL130, UL83; 8-9: gB, gM, gN, gH, gL, UL128, UL131a, UL83; 8-10: gB, gM, gN, gH, gL, UL130, UL131a, UL83; 8-11: gB, gM, gN, gH, gO, UL128, UL130, UL131a; 8-12: gB, gM, gN, gH, gO, UL128, UL130, UL83; 8-13: gB, gM, gN, gH, gO, UL128, UL131a, UL83; 8-14: gB, gM, gN, gH, gO, UL130, UL131a, UL83; 8-15: gB, gM, gN, gH, UL128, UL130, UL131a, UL83; 8-16: gB, gM, gN, gL, gO, UL128, UL130, UL131a; 8-17: gB, gM, gN, gL, gO, UL128, UL130, UL83; 8-18: gB, gM, gN, gL, gO, UL128, UL131a, UL83; 8-19: gB, gM, gN, gL, gO, UL130, UL131a, UL83; 8-20: gB, gM, gN, gL, UL128, UL130, UL131a, UL83; 8-21: gB, gM, gN, gO, UL128, UL130, UL131a, UL83; 8-22: gB, gM, gH, gL, gO, UL128, UL130, UL131a; 8-23: gB, gM, gH, gL, gO, UL128, UL130, UL83; 8-24: gB, gM, gH, gL, gO, UL128, UL131a, UL83; 8-25: gB, gM, gH, gL, gO, UL130, UL131a, UL83; 8-26: gB, gM, gH, gL, UL128, UL130, UL131a, UL83; 8-27: gB, gM, gH, gO, UL128, UL130, UL131a, UL83; 8-28: gB, gM, gL, gO, UL128, UL130, UL131a, UL83; 8-29: gB, gN, gH, gL, gO, UL128, UL130, UL131a; 8-30: gB, gN, gH, gL, gO, UL128, UL130, UL83; 8-31: gB, gN, gH, gL, gO, UL128, UL131a, UL83; 8-32: gB, gN, gH, gL, gO, UL130, UL131a, UL83; 8-33: gB, gN, gH, gL, UL128, UL130, UL131a, UL83; 8-34: gB, gN, gH, gO, UL128, UL130, UL131a, UL83; 8-35: gB, gN, gL, gO, UL128, UL130, UL131a, UL83; 8-36: gB, gH, gL, gO, UL128, UL130, UL131a, UL83; 8-37: gM, gN, gH, gL, gO, UL128, UL130, UL131a; 7-x: 8-38: gM, gN, gH, gL, gO, UL128, UL130, UL83; 8-39: gM, gN, gH, gL, gO, UL128, UL131a, UL83; 8-40: gM, gN, gH, gL, gO, UL130, UL131a, UL83; 8-41: gM, gN, gH, gL, gL, UL128, UL130, UL131a, UL83; 8-42: gM, gN, gH, gL, gO, UL128, UL130, UL131a, UL83; 8-43: gM, gN, gL, gO, UL128, UL130, UL131a, UL83; 8-44: gM, gH, gL, gO, UL128, UL130, UL131a, UL83; and 8-45: gN, gH, gL, gO, UL128, UL130, UL131a, UL83. In some embodiments, these vaccines com-

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prise one or more of the coding sequences encoding each of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a that have sequences selected from the group consisting of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 and 60. In some embodiments, one or more of the coding sequences is selected from the group consisting of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 and 59. In some embodiments, one or more of the coding sequences in a vaccine is selected from the group consisting of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 and 59.

Example 5

In some embodiments, a composition comprising coding sequences for seven of: gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83, or multiple compositions which collectively comprise coding sequences for seven of: gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83 are administered. The composition may comprises coding sequences of seven of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83, or combinations of compositions that collectively comprise coding sequences of seven of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83. The following combinations 7-1 to 7-120 may be present in an seven antigen vaccine: 7-1: gB, gM, gN, gH, gL, gO, UL128; 7-2: gB, gM, gN, gH, gL, gO, UL130; 7-3: gB, gM, gN, gH, gL, gO, UL131a; 7-4: gB, gM, gN, gH, gL, gO, UL83; 7-5: gB, gM, gN, gH, gL, UL128, UL130; 7-6: gB, gM, gN, gH, gL, UL128, UL131a; 7-7: gB, gM, gN, gH, gL, UL128, UL83; 7-8: gB, gM, gN, gH, gL, UL130, UL131a; 7-9: gB, gM, gN, gH, gL, UL130, UL83; 7-10: gB, gM, gN, gH, gL, UL131a, UL83; 7-11: gB, gM, gN, gH, gO, UL128, UL130; 7-12: gB, gM, gN, gH, gO, UL128, UL131a; 7-13: gB, gM, gN, gH, gO, UL128, UL83; 7-14: gB, gM, gN, gH, gO, UL130, UL131a; 7-15: gB, gM, gN, gH, gO, UL130, UL83; 7-16: gB, gM, gN, gH, gO, UL131a, UL83; 7-17: gB, gM, gN, gH, UL128, UL130, UL131a; 7-18: gB, gM, gN, gH, UL128, UL130, UL83; 7-19: gB, gM, gN, gH, UL128, UL130, UL131a; 7-20: gB, gM, gN, gH, UL128, UL130, UL83; 7-21: gB, gM, gN, gH, UL128, UL131a, UL83; 7-22: gB, gM, gN, gH, UL130, UL131a, UL83; 7-23: gB, gM, gN, gL, gO, UL128, UL130; 7-24: gB, gM, gN, gL, gO, UL128, UL131a; 7-25: gB, gM, gN, gL, gO, UL128, UL83; 7-26: gB, gM, gN, gL, gO, UL130, UL131a; 7-27: gB, gM, gN, gL, gO, UL130, UL83; 7-28: gB, gM, gN, gL, gO, UL131a, UL83; 7-29: gB, gM, gN, gL, UL128, UL130, UL131a; 7-30: gB, gM, gN, gL, UL128, UL130, UL83; 7-31: gB, gM, gN, gL, UL128, UL130, UL131a; 7-32: gB, gM, gN, gL, UL128, UL130, UL83; 7-33: gB, gM, gN, gL, UL128, UL131a, UL83; 7-34: gB, gM, gN, gL, UL130, UL131a, UL83; 7-35: gB, gM, gN, gO, UL128, UL130, UL131a; 7-36: gB, gM, gN, gO, UL128, UL130, UL83; 7-37: gB, gM, gN, gO, UL128, UL131a, UL83; 7-38: gB, gM, gN, gO, UL130, UL131a, UL83; 7-39: gB, gM, gN, UL128, UL130, UL131a, UL83; 7-40: gB, gM, gH, gL, gO, UL128, UL130; 7-41: gB, gM, gH, gL, gO, UL128, UL131a; 7-42: gB, gM, gH, gL, gO, UL128, UL83; 7-43: gB, gM, gH, gL, gO, UL130, UL131a; 7-44: gB, gM, gH, gL, gO, UL130, UL83; 7-45: gB, gM, gH, gL, gO, UL131a, UL83; 7-46: gB, gM, gH, gO, UL128, UL130, UL131a; 7-47: gB, gM, gH, gO, UL128, UL130, UL83; 7-48: gB, gM, gH, gO, UL128, UL131a, UL83; 7-49: gB, gM, gH, gO, UL130, UL131a, UL83; 7-50: gB, gM, gH, UL128, UL130, UL131a, UL83; 7-51: gB, gM, gL, gO, UL128, UL130, UL131a; 7-52: gB,

gM, gL, gO, UL128, UL130, UL83; 7-53: gB, gM, gL, gO, UL128, UL131a, UL83; 7-54: gB, gM, gL, gO, UL130, UL131a, UL83; 7-55: gB, gM, gL, UL128, UL130, UL131a, UL83; 7-56: gB, gM, gO, UL128, UL130, UL131a, UL83; 7-57: gB, gN, gH, gL, gO, UL128, UL130; 7-58: gB, gN, gH, gL, gO, UL128, UL131a; 7-59: gB, gN, gH, gL, gO, UL128, UL83; 7-60: gB, gN, gH, gL, gO, UL130, UL131a; 7-61: gB, gN, gH, gL, gO, UL130, UL83; 7-62: gB, gN, gH, gL, gO, UL131a, UL83; 7-63: gB, gN, gH, gL, UL128, UL130, UL131a; 7-64: gB, gN, gH, gL, UL128, UL130, UL83; 7-65: gB, gN, gH, gL, UL128, UL131a, UL83; 7-66: gB, gN, gH, gL, UL130, UL131a, UL83; 7-67: gB, gN, gH, gO, UL128, UL130, UL131a; 7-68: gB, gN, gH, gO, UL128, UL130, UL83; 7-69: gB, gN, gH, gO, UL128, UL131a, UL83; 7-70: gB, gN, gH, gO, UL130, UL131a, UL83; 7-71: gB, gN, gH, UL128, UL130, UL131a, UL83; 7-72: gB, gN, gL, gO, UL128, UL130, UL131a; 7-73: gB, gN, gL, gO, UL128, UL130, UL83; 7-74: gB, gN, gL, gO, UL128, UL131a, UL83; 7-75: gB, gN, gL, gO, UL130, UL131a, UL83; 7-76: gB, gN, gL, UL128, UL130, UL131a, UL83; 7-77: gB, gN, gO, UL128, UL130, UL131a, UL83; 7-78: gB, gH, gL, gO, UL128, UL130, UL131a; 7-79: gB, gH, gL, gO, UL128, UL130, UL83; 7-80: gB, gH, gL, gO, UL128, UL131a, UL83; 7-81: gB, gH, gL, gO, UL130, UL131a, UL83; 7-82: gB, gH, gL, UL128, UL130, UL131a, UL83; 7-83: gB, gH, gO, UL128, UL130, UL131a, UL83; 7-84: gB, gL, gO, UL128, UL130, UL131a, UL83; 7-85: gM, gN, gH, gL, gO, UL128, UL130; 7-86: gM, gN, gH, gL, gO, UL128, UL131a; 7-87: gM, gN, gH, gL, gO, UL128, UL83; 7-88: gM, gN, gH, gL, gO, UL130, UL131a; 7-89: gM, gN, gH, gL, gO, UL130, UL83; 7-90: gM, gN, gH, gL, gO, UL131a, UL83; 7-91: gM, gN, gH, gL, gL, UL128, UL130, UL131a; 7-92: gM, gN, gH, gL, gL, UL128, UL130, UL83; 7-93: gM, gN, gH, gL, gL, UL128, UL131a, UL83; 7-94: gM, gN, gH, gL, gL, UL130, UL131a, UL83; 7-95: gM, gN, gH, gL, gO, UL128, UL130, UL131a; 7-96: gM, gN, gH, gL, gO, UL128, UL130, UL83; 7-97: gM, gN, gH, gL, gO, UL128, UL131a, UL83; 7-98: gM, gN, gH, gL, gO, UL130, UL131a, UL83; 7-99: gM, gN, gH, gL, UL128, UL130, UL131a, UL83; 7-100: gM, gN, gL, gO, UL128, UL130, UL131a; 7-101: gM, gN, gL, gO, UL128, UL130, UL83; 7-102: gM, gN, gL, gO, UL128, UL131a, UL83; 7-103: gM, gN, gL, gO, UL130, UL131a, UL83; 7-104: gM, gN, gL, UL128, UL130, UL131a, UL83; 7-105: gM, gN, gO, UL128, UL130, UL131a, UL83; 7-106: gM, gH, gL, gO, UL128, UL130, UL131a; 7-107: gM, gH, gL, gO, UL128, UL130, UL83; 7-108: gM, gH, gL, gO, UL128, UL131a, UL83; 7-109: gM, gH, gL, gO, UL130, UL131a, UL83; 7-110: gM, gH, gL, UL128, UL130, UL131a, UL83; 7-111: gM, gH, gO, UL128, UL130, UL131a, UL83; 7-112: gM, gL, gO, UL128, UL130, UL131a, UL83; 7-113: gN, gH, gL, gO, UL128, UL130, UL131a; 7-114: gN, gH, gL, gO, UL128, UL130, UL83; 7-115: gN, gH, gL, gO, UL128, UL131a, UL83; 7-116: gN, gH, gL, gO, UL130, UL131a, UL83; 7-117: gN, gH, gL, UL128, UL130, UL131a, UL83; 7-118: gN, gH, gO, UL128, UL130, UL131a, UL83; 7-119: gN, gL, gO, UL128, UL130, UL131a, UL83; 7-120: gH, gL, gO, UL128, UL130, UL131a, UL83. In some embodiments, these vaccines comprise one or more of the coding sequences encoding each of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a that have sequences selected from the group consisting of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 and 60. In some embodiments, one or more of the coding sequences is selected from the group consisting of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55,

57 and 59. In some embodiments, one or more of the coding sequences in a vaccine is selected from the group consisting of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 and 59.

Example 6

In some embodiments, a composition comprising coding sequences for six of: gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83, or multiple compositions which collectively comprise coding sequences for six of: gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83 are administered. The composition may comprises coding sequences of six of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83, or combinations of compositions that collectively comprise coding sequences of six of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83. The following combinations 6-1 to 6-210 may be present in an seven antigen vaccine: 6-1: gB, gM, gN, gH, gL, gO; 6-2: gB, gM, gN, gH, gL, UL128; 6-3: gB, gM, gN, gH, gL, UL130; 6-4: gB, gM, gN, gH, gL, UL131a; 6-5: gB, gM, gN, gH, gL, UL83; 6-6: gB, gM, gN, gH, gO, UL128; 6-7: gB, gM, gN, gH, gO, UL130; 6-8: gB, gM, gN, gH, gO, UL131a; 6-9: gB, gM, gN, gH, gO, UL83; 6-10: gB, gM, gN, gH, UL128, UL130; 6-11: gB, gM, gN, gH, UL128, UL131a; 6-12: gB, gM, gN, gH, UL128, UL83; 6-13: gB, gM, gN, gH, UL130, UL131a; 6-14: gB, gM, gN, gH, UL130, UL83; 6-15: gB, gM, gN, gH, UL131a, UL83; 6-16: gB, gM, gN, gL, gO, UL128; 6-17: gB, gM, gN, gL, gO, UL130; 6-18: gB, gM, gN, gL, gO, UL131a; 6-19: gB, gM, gN, gL, gO, UL83; 6-20: gB, gM, gN, gL, UL128, UL130; 6-21: gB, gM, gN, gL, UL128, UL131a; 6-22: gB, gM, gN, gL, UL128, UL83; 6-23: gB, gM, gN, gL, UL130, UL131a; 6-24: gB, gM, gN, gL, UL130, UL83; 6-25: gB, gM, gN, gL, UL131a, UL83; 6-26: gB, gM, gN, gO, UL128, UL130; 6-27: gB, gM, gN, gO, UL128, UL131a; 6-28: gB, gM, gN, gO, UL128, UL83; 6-29: gB, gM, gN, gO, UL130, UL131a; 6-30: gB, gM, gN, gO, UL130, UL83; 6-31: gB, gM, gN, gO, UL131a, UL83; 6-32: gB, gM, gN, UL128, UL130, UL131a; 6-33: gB, gM, gN, UL128, UL130, UL83; 6-34: gB, gM, gN, UL128, UL131a, UL83; 6-35: gB, gM, gN, UL130, UL131a, UL83; 6-36: gB, gM, gH, gL, gO, UL128; 6-37: gB, gM, gH, gL, gO, UL130; 6-38: gB, gM, gH, gL, gO, UL131a; 6-39: gB, gM, gH, gL, gO, UL83; 6-40: gB, gM, gH, gL, UL128, UL130; 6-41: gB, gM, gH, gL, UL128, UL131a; 6-42: gB, gM, gH, gL, UL128, UL83; 6-43: gB, gM, gH, gL, UL130, UL131a; 6-44: gB, gM, gH, gL, UL130, UL83; 6-45: gB, gM, gH, gL, UL131a, UL83; 6-46: gB, gM, gH, gO, UL128, UL130; 6-47: gB, gM, gH, gO, UL128, UL131a; 6-48: gB, gM, gH, gO, UL128, UL83; 6-49: gB, gM, gH, gO, UL130, UL131a; 6-50: gB, gM, gH, gO, UL130, UL83; 6-51: gB, gM, gH, gO, UL131a, UL83; 6-52: gB, gM, gH, UL128, UL130, UL131a; 6-53: gB, gM, gH, UL128, UL130, UL83; 6-54: gB, gM, gH, UL128, UL131a, UL83; 6-55: gB, gM, gH, UL130, UL131a, UL83; 6-56: gB, gM, gL, gO, UL128, UL130; 6-57: gB, gM, gL, gO, UL128, UL131a; 6-58: gB, gM, gL, gO, UL128, UL83; 6-59: gB, gM, gL, gO, UL130, UL131a; 6-60: gB, gM, gL, gO, UL130, UL83; 6-61: gB, gM, gL, gO, UL131a, UL83; 6-62: gB, gM, gL, UL128, UL130, UL131a; 6-63: gB, gM, gL, UL128, UL130, UL83; 6-64: gB, gM, gL, UL128, UL131a, UL83; 6-65: gB, gM, gL, UL130, UL131a, UL83; 6-66: gB, gM, gO, UL128, UL130, UL83; 6-67: gB, gM, gO, UL128, UL130, UL83; 6-68: gB, gM, gO, UL128, UL131a, UL83; 6-69: gB, gM, gO, UL130, UL131a, UL83; 6-70: gB, gM, UL128, UL130, UL131a, UL83; 6-71: gB, gN, gH, gL, gO, UL128; 6-72:

gB, gN, gH, gL, gO, UL130; 6-73: gB, gN, gH, gL, gO, UL131a; 6-74: gB, gN, gH, gL, gO, UL83; 6-75: gB, gN, gH, gL, UL128, UL130; 6-76: gB, gN, gH, gL, UL128, UL131a; 6-77: gB, gN, gH, gL, UL128, UL83; 6-78: gB, gN, gH, gL, UL130, UL131a; 6-79: gB, gN, gH, gL, UL130, UL83; 6-80: gB, gN, gH, gL, UL131a, UL83; 6-81: gB, gN, gH, gO, UL128, UL130; 6-82: gB, gN, gH, gO, UL128, UL131a; 6-83: gB, gN, gH, gO, UL128, UL83; 6-84: gB, gN, gH, gO, UL130, UL131a; 6-85: gB, gN, gH, gO, UL130, UL83; 6-86: gB, gN, gH, gO, UL131a, UL83; 6-87: gB, gN, gH, UL128, UL130, UL131a; 6-88: gB, gN, gH, UL128, UL130, UL83; 6-89: gB, gN, gH, UL128, UL131a, UL83; 6-90: gB, gN, gH, UL130, UL131a, UL83; 6-91: gB, gN, gL, gO, UL128, UL130; 6-92: gB, gN, gL, gO, UL128, UL131a; 6-93: gB, gN, gL, gO, UL128, UL83; 6-94: gB, gN, gL, gO, UL130, UL131a; 6-95: gB, gN, gL, gO, UL130, UL83; 6-96: gB, gN, gL, gO, UL131a, UL83; 6-97: gB, gN, gL, UL128, UL130, UL131a; 6-98: gB, gN, gL, UL128, UL130, UL83; 6-99: gB, gN, gL, UL128, UL131a, UL83; 6-100: gB, gN, gL, UL130, UL131a, UL83; 6-101: gB, gN, gO, UL128, UL130, UL131a; 6-102: gB, gN, gO, UL128, UL130, UL83; 6-103: gB, gN, gO, UL128, UL131a, UL83; 6-104: gB, gN, gO, UL130, UL131a, UL83; 6-105: gB, gN, UL128, UL130, UL131a, UL83; 6-106: gB, gH, gL, gO, UL128, UL130; 6-107: gB, gH, gL, gO, UL128, UL131a; 6-108: gB, gH, gL, gO, UL128, UL83; 6-109: gB, gH, gL, gO, UL130, UL131a; 6-110: gB, gH, gL, gO, UL130, UL83; 6-111: gB, gH, gL, gO, UL131a, UL83; 6-112: gB, gH, gL, UL128, UL130, UL131a; 6-113: gB, gH, gL, UL128, UL130, UL83; 6-114: gB, gH, gL, UL128, UL131a, UL83; 6-115: gB, gH, gL, UL130, UL131a, UL83; 6-116: gB, gH, gO, UL128, UL130, UL131a; 6-117: gB, gH, gO, UL128, UL130, UL83; 6-118: gB, gH, gO, UL128, UL131a, UL83; 6-119: gB, gH, gO, UL130, UL131a, UL83; 6-120: gB, gH, UL128, UL130, UL131a, UL83; 6-121: gB, gL, gO, UL128, UL130, UL131a; 6-122: gB, gL, gO, UL128, UL130, UL83; 6-123: gB, gL, gO, UL128, UL131a, UL83; 6-124: gB, gL, gO, UL130, UL131a, UL83; 6-125: gB, gL, UL128, UL130, UL131a, UL83; 6-126: gB, gO, UL128, UL130, UL131a, UL83; 6-127: gM, gN, gH, gL, gO, UL128; 6-128: gM, gN, gH, gL, gO, UL130; 6-129: gM, gN, gH, gL, gO, UL131a; 6-130: gM, gN, gH, gL, gO, UL83; 6-131: gM, gN, gH, gL, UL128, UL130; 6-132: gM, gN, gH, gL, UL128, UL131a; 6-133: gM, gN, gH, gL, UL128, UL83; 6-134: gM, gN, gH, gL, UL130, UL131a; 6-135: gM, gN, gH, gL, UL130, UL83; 6-136: gM, gN, gH, gL, UL131a, UL83; 6-137: gM, gN, gH, gO, UL128, UL130; 6-138: gM, gN, gH, gO, UL128, UL131a; 6-139: gM, gN, gH, gO, UL128, UL83; 6-140: gM, gN, gH, gO, UL130, UL131a; 6-141: gM, gN, gH, gO, UL130, UL83; 6-142: gM, gN, gH, gO, UL131a, UL83; 6-143: gM, gN, gH, UL128, UL130, UL131a; 6-144: gM, gN, gH, UL128, UL130, UL83; 6-145: gM, gN, gH, UL128, UL131a, UL83; 6-146: gM, gN, gH, UL130, UL131a, UL83; 6-147: gM, gN, gL, gO, UL128, UL130; 6-148: gM, gN, gL, gO, UL128, UL131a; 6-149: gM, gN, gL, gO, UL128, UL83; 6-150: gM, gN, gL, gO, UL130, UL131a; 6-151: gM, gN, gL, gO, UL130, UL83; 6-152: gM, gN, gL, gO, UL131a, UL83; 6-153: gM, gN, gL, UL128, UL130, UL131a; 6-154: gM, gN, gL, UL128, UL130, UL83; 6-155: gM, gN, gL, UL128, UL131a, UL83; 6-156: gM, gN, gL, UL130, UL131a, UL83; 6-157: gM, gN, gO, UL128, UL130, UL131a; 6-158: gM, gN, gO, UL128, UL130, UL83; 6-159: gM, gN, gO, UL128, UL131a, UL83; 6-160: gM, gN, gO, UL130, UL131a, UL83; 6-161: gM, gN, UL128, UL130, UL131a, UL83; 6-162: gM, gH, gL, gO, UL128, UL130; 6-163: gM, gH, gL, gO, UL128, UL131a; 6-164: gM, gH, gL, gO, UL128, UL83; 6-165: gM, gH, gL,

gO, UL130, UL131a; 6-166: gM, gH, gL, gO, UL130, UL83; 6-167: gM, gH, gL, gO, UL131a, UL83; 6-168: gM, gH, gL, UL128, UL130, UL131a; 6-169: gM, gH, gL, UL128, UL130, UL83; 6-170: gM, gH, gL, UL128, UL131a, UL83; 6-171: gM, gH, gL, UL130, UL131a, UL83; 6-172: gM, gH, gO, UL128, UL130, UL131a; 6-173: gM, gH, gO, UL128, UL130, UL83; 6-174: gM, gH, gO, UL128, UL131a, UL83; 6-175: gM, gH, gO, UL130, UL131a, UL83; 6-176: gM, gH, UL128, UL130, UL131a, UL83; 6-177: gM, gL, gO, UL128, UL130, UL131a; 6-178: gM, gL, gO, UL128, UL130, UL83; 6-179: gM, gL, gO, UL128, UL131a, UL83; 6-180: gM, gL, gO, UL130, UL131a, UL83; 6-181: gM, gL, UL128, UL130, UL131a, UL83; 6-182: gM, gO, UL128, UL130, UL131a, UL83; 6-183: gN, gH, gL, gO, UL128, UL130; 6-184: gN, gH, gL, gO, UL128, UL131a; 6-185: gN, gH, gL, gO, UL128, UL83; 6-186: gN, gH, gL, gO, UL130, UL131a; 6-187: gN, gH, gL, gO, UL130, UL83; 6-188: gN, gH, gL, gO, UL131a, UL83; 6-189: gN, gH, gL, UL128, UL130, UL131a; 6-190: gN, gH, gL, UL128, UL130, UL83; 6-191: gN, gH, gL, UL128, UL131a, UL83; 6-192: gN, gH, gL, UL130, UL131a, UL83; 6-193: gN, gH, gO, UL128, UL130, UL131a; 6-194: gN, gH, gO, UL128, UL130, UL83; 6-195: gN, gH, gO, UL128, UL131a, UL83; 6-196: gN, gH, gO, UL130, UL131a, UL83; 6-197: gN, gH, UL128, UL130, UL131a, UL83; 6-198: gN, gL, gO, UL128, UL130, UL131a; 6-199: gN, gL, gO, UL128, UL130, UL83; 6-200: gN, gL, gO, UL128, UL131a, UL83; 6-201: gN, gL, gO, UL130, UL131a, UL83; 6-202: gN, gL, UL128, UL130, UL131a, UL83; 6-203: gN, gO, UL128, UL130, UL131a, UL83; 6-204: gH, gL, gO, UL128, UL130, UL131a; 6-205: gH, gL, gO, UL128, UL130, UL83; 6-206: gH, gL, gO, UL128, UL131a, UL83; 6-207: gH, gL, gO, UL130, UL131a, UL83; 6-208: gH, gL, UL128, UL130, UL131a, UL83; 6-209: gH, gO, UL128, UL130, UL131a, UL83; and 6-210: gL, gO, UL128, UL130, UL131a, UL83. In some embodiments, these vaccines comprise one or more of the coding sequences encoding each of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a that have sequences selected from the group consisting of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 and 60. In some embodiments, one or more of the coding sequences is selected from the group consisting of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 and 59. In some embodiments, one or more of the coding sequences in a vaccine is selected from the group consisting of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 and 59.

Example 7

In some embodiments, a composition comprising coding sequences for five of: gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83, or multiple compositions which collectively comprise coding sequences for five of: gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83 are administered. The composition which comprises coding sequences of five of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83, or combinations of compositions that collectively comprise coding sequences of five of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83 are referred to as "five antigen vaccines". The following combinations 5-1 to 5-252 may be present in an five antigen vaccine: 5-1: gB, gM, gN, gH, gL; 5-2: gB, gM, gN, gH, gO; 5-3: gB, gM, gN, gH, UL128; 5-4: gB, gM, gN, gH, UL130; 5-5: gB, gM, gN, gH, UL131a; 5-6: gB, gM, gN, gH, UL83; 5-7: gB, gM, gN, gL,

gO; 5-8: gB, gM, gN, gL, UL128; 5-9: gB, gM, gN, gL, UL130; 5-10: gB, gM, gN, gL, UL131a; 5-11: gB, gM, gN, gL, UL83; 5-12: gB, gM, gN, gO, UL128; 5-13: gB, gM, gN, gO, UL130; 5-14: gB, gM, gN, gO, UL131a; 5-15: gB, gM, gN, gO, UL83; 5-16: gB, gM, gN, UL128, UL130; 5-17: gB, gM, gN, UL128, UL131a; 5-18: gB, gM, gN, UL128, UL83; 5-19: gB, gM, gN, UL130, UL131a; 5-20: gB, gM, gN, UL130, UL83; 5-21: gB, gM, gN, UL131A, UL83; 5-22: gB, gM, gH, gL, gO; 5-23: gB, gM, gH, gL, UL128; 5-24: gB, gM, gH, gL, UL130; 5-25: gB, gM, gH, gL, UL131a; 5-26: gB, gM, gH, gL, UL83; 5-27: gB, gM, gH, gO, UL128; 5-28: gB, gM, gH, gO, UL130; 5-29: gB, gM, gH, gO, UL131a; 5-30: gB, gM, gH, gO, UL83; 5-31: gB, gM, gH, UL128, UL130; 5-32: gB, gM, gH, UL128, UL131a; 5-33: gB, gM, gH, UL128, UL83; 5-34: gB, gM, gH, UL130, UL131a; 5-35: gB, gM, gH, UL130, UL83; 5-36: gB, gM, gH, UL131A, UL83; 5-37: gB, gM, gL, gO, UL128; 5-38: gB, gM, gL, gO, UL130; 5-39: gB, gM, gL, gO, UL131a; 5-40: gB, gM, gL, gO, UL83; 5-41: gB, gM, gL, UL128, UL130; 5-42: gB, gM, gL, UL128, UL131a; 5-43: gB, gM, gL, UL128, UL83; 5-44: gB, gM, gL, UL130, UL131a; 5-45: gB, gM, gL, UL130, UL83; 5-46: gB, gM, gL, UL131A, UL83; 5-47: gB, gM, gO, UL128, UL130; 5-48: gB, gM, gO, UL128, UL131a; 5-49: gB, gM, gO, UL128, UL83; 5-50: gB, gM, gO, UL130, UL131a; 5-51: gB, gM, gO, UL130, UL83; 5-52: gB, gM, gO, UL131A, UL83; 5-53: gB, gM, UL128, UL130, UL131a; 5-54: gB, gM, UL128, UL130, UL83; 5-55: gB, gM, UL128, UL131A, UL83; 5-56: gB, gM, UL130, UL131A, UL83; 5-57: gB, gN, gH, gL, gO; 5-58: gB, gN, gH, gL, UL128; 5-59: gB, gN, gH, gL, UL130; 5-60: gB, gN, gH, gL, UL131a; 5-61: gB, gN, gH, gL, UL83; 5-62: gB, gN, gH, gO, UL128; 5-63: gB, gN, gH, gO, UL130; 5-64: gB, gN, gH, gO, UL131a; 5-65: gB, gN, gH, gO, UL83; 5-66: gB, gN, gH, UL128, UL130; 5-67: gB, gN, gH, UL128, UL131a; 5-68: gB, gN, gH, UL128, UL83; 5-69: gB, gN, gH, UL130, UL131a; 5-70: gB, gN, gH, UL130, UL83; 5-71: gB, gN, gH, UL131A, UL83; 5-72: gB, gN, gL, gO, UL128; 5-73: gB, gN, gL, gO, UL130; 5-74: gB, gN, gL, gO, UL131a; 5-75: gB, gN, gL, gO, UL83; 5-76: gB, gN, gL, UL128, UL130; 5-77: gB, gN, gL, UL128, UL131a; 5-78: gB, gN, gL, UL128, UL83; 5-79: gB, gN, gL, UL130, UL131a; 5-80: gB, gN, gL, UL130, UL83; 5-81: gB, gN, gL, UL131A, UL83; 5-82: gB, gN, gO, UL128, UL130; 5-83: gB, gN, gO, UL128, UL131a; 5-84: gB, gN, gO, UL128, UL83; 5-85: gB, gN, gO, UL130, UL131a; 5-86: gB, gN, gO, UL130, UL83; 5-87: gB, gN, gO, UL131A, UL83; 5-88: gB, gN, UL128, UL130, UL131a; 5-89: gB, gN, UL128, UL130, UL83; 5-90: gB, gN, UL128, UL131A, UL83; 5-91: gB, gN, UL130, UL131A, UL83; 5-92: gB, gH, gL, gO, UL128; 5-93: gB, gH, gL, gO, UL130; 5-94: gB, gH, gL, gO, UL131a; 5-95: gB, gH, gL, gO, UL83; 5-96: gB, gH, gL, UL128, UL130; 5-97: gB, gH, gL, UL128, UL131a; 5-98: gB, gH, gL, UL128, UL83; 5-99: gB, gH, gL, UL130, UL131a; 5-100: gB, gH, gL, UL130, UL83; 5-101: gB, gH, gL, UL131A, UL83; 5-102: gB, gH, gO, UL128, UL130; 5-103: gB, gH, gO, UL128, UL131a; 5-104: gB, gH, gO, UL128, UL83; 5-105: gB, gH, gO, UL130, UL131a; 5-106: gB, gH, gO, UL130, UL83; 5-107: gB, gH, gO, UL131A, UL83; 5-108: gB, gH, UL128, UL130, UL131a; 5-109: gB, gH, UL128, UL130, UL83; 5-110: gB, gH, UL128, UL131A, UL83; 5-111: gB, gH, UL130, UL131A, UL83; 5-112: gB, gL, gO, UL128, UL130; 5-113: gB, gL, gO, UL128, UL131a; 5-114: gB, gL, gO, UL128, UL83; 5-115: gB, gL, gO, UL130, UL131a; 5-116: gB, gL, gO, UL130, UL83; 5-117: gB, gL, gO, UL131A, UL83; 5-118: gB, gL, UL128, UL130, UL131a; 5-119: gB, gL, UL128, UL130,

UL83; 5-120: gB, gL, UL128, UL131A, UL83; 5-121: gB, gL, UL130, UL131A, UL83; 5-122: gB, gO, UL128, UL130, UL131a; 5-123: gB, gO, UL128, UL130, UL83; 5-124: gB, gO, UL128, UL131A, UL83; 5-125: gB, gO, UL130, UL131A, UL83; 5-126: gB, UL128, UL130, UL131A, UL83; 5-127: gM, gN, gH, gL, gO; 5-128: gM, gN, gH, gL, UL128; 5-129: gM, gN, gH, gL, UL130; 5-130: gM, gN, gH, gL, UL131a; 5-131: gM, gN, gH, gL, UL83; 5-132: gM, gN, gH, gO, UL128; 5-133: gM, gN, gH, gO, UL130; 5-134: gM, gN, gH, gO, UL131a; 5-135: gM, gN, gH, gO, UL83; 5-136: gM, gN, gH, UL128, UL130; 5-137: gM, gN, gH, UL128, UL131a; 5-138: gM, gN, gH, UL128, UL83; 5-139: gM, gN, gH, UL130, UL131a; 5-140: gM, gN, gH, UL130, UL83; 5-141: gM, gN, gH, UL131A, UL83; 5-142: gM, gN, gL, gO, UL128; 5-143: gM, gN, gL, gO, UL130; 5-144: gM, gN, gL, gO, UL131a; 5-145: gM, gN, gL, gO, UL83; 5-146: gM, gN, gL, UL128, UL130; 5-147: gM, gN, gL, UL128, UL131a; 5-148: gM, gN, gL, UL128, UL83; 5-149: gM, gN, gL, UL130, UL131a; 5-150: gM, gN, gL, UL130, UL83; 5-151: gM, gN, gL, UL131A, UL83; 5-152: gM, gN, gO, UL128, UL130; 5-153: gM, gN, gO, UL128, UL131a; 5-154: gM, gN, gO, UL128, UL83; 5-155: gM, gN, gO, UL130, UL131a; 5-156: gM, gN, gO, UL130, UL83; 5-157: gM, gN, gO, UL131A, UL83; 5-158: gM, gN, UL128, UL130, UL131a; 5-159: gM, gN, UL128, UL130, UL83; 5-160: gM, gN, UL128, UL131A, UL83; 5-161: gM, gN, UL130, UL131A, UL83; 5-162: gM, gH, gL, gO, UL128; 5-163: gM, gH, gL, gO, UL130; 5-164: gM, gH, gL, gO, UL131a; 5-165: gM, gH, gL, gO, UL83; 5-166: gM, gH, gL, UL128, UL130; 5-167: gM, gH, gL, UL128, UL131a; 5-168: gM, gH, gL, UL128, UL83; 5-169: gM, gH, gL, UL130, UL131a; 5-170: gM, gH, gL, UL130, UL83; 5-171: gM, gH, gL, UL131A, UL83; 5-172: gM, gH, gO, UL128, UL130; 5-173: gM, gH, gO, UL128, UL131a; 5-174: gM, gH, gO, UL128, UL83; 5-175: gM, gH, gO, UL130, UL131a; 5-176: gM, gH, gO, UL130, UL83; 5-177: gM, gH, gO, UL131A, UL83; 5-178: gM, gH, UL128, UL130, UL131a; 5-179: gM, gH, UL128, UL130, UL83; 5-180: gM, gH, UL128, UL131A, UL83; 5-181: gM, gH, UL130, UL131A, UL83; 5-182: gM, gL, gO, UL128, UL130; 5-183: gM, gL, gO, UL128, UL131a; 5-184: gM, gL, gO, UL128, UL83; 5-185: gM, gL, gO, UL130, UL131a; 5-186: gM, gL, gO, UL130, UL83; 5-187: gM, gL, gO, UL131A, UL83; 5-188: gM, gL, UL128, UL130, UL131a; 5-189: gM, gL, UL128, UL130, UL83; 5-190: gM, gL, UL128, UL131A, UL83; 5-191: gM, gL, UL130, UL131A, UL83; 5-192: gM, gO, UL128, UL130, UL131a; 5-193: gM, gO, UL128, UL130, UL83; 5-194: gM, gO, UL128, UL131A, UL83; 5-195: gM, gO, UL130, UL131A, UL83; 5-196: gM, UL128, UL130, UL131A, UL83; 5-197: gN, gH, gL, gO, UL128; 5-198: gN, gH, gL, gO, UL130; 5-199: gN, gH, gL, gO, UL131a; 5-200: gN, gH, gL, gO, UL83; 5-201: gN, gH, gL, UL128, UL130; 5-202: gN, gH, gL, UL128, UL131a; 5-203: gN, gH, gL, UL128, UL83; 5-204: gN, gH, gL, UL130, UL131a; 5-205: gN, gH, gL, UL130, UL83; 5-206: gN, gH, gL, UL131A, UL83; 5-207: gN, gH, gO, UL128, UL130; 5-208: gN, gH, gO, UL128, UL131a; 5-209: gN, gH, gO, UL128, UL83; 5-210: gN, gH, gO, UL130, UL131a; 5-211: gN, gH, gO, UL130, UL83; 5-212: gN, gH, gO, UL131A, UL83; 5-213: gN, gH, UL128, UL130, UL131a; 5-214: gN, gH, UL128, UL130, UL83; 5-215: gN, gH, UL128, UL131A, UL83; 5-216: gN, gH, UL130, UL131A, UL83; 5-217: gN, gL, gO, UL128, UL130; 5-218: gN, gL, gO, UL128, UL131a; 5-219: gN, gL, gO, UL128, UL83; 5-220: gN, gL, gO, UL130, UL131a; 5-221: gN, gL, gO, UL130, UL83; 5-222: gN, gL, gO, UL131A, UL83; 5-223: gN, gL, UL128, UL130, UL131a; 5-224: gN, gL,

UL128, UL130, UL83; 5-225: gN, gL, UL128, UL131A, UL83; 5-226: gN, gL, UL130, UL131A, UL83; 5-227: gN, gO, UL128, UL130, UL131a; 5-228: gN, gO, UL128, UL130, UL83; 5-229: gN, gO, UL128, UL131A, UL83; 5-230: gN, gO, UL130, UL131A, UL83; 5-231: gN, UL128, UL130, UL131A, UL83; 5-232: gH, gL, gO, UL128, UL130; 5-233: gH, gL, gO, UL128, UL131a; 5-234: gH, gL, gO, UL128, UL83; 5-235: gH, gL, gO, UL130, UL131a; 5-236: gH, gL, gO, UL130, UL83; 5-237: gH, gL, gO, UL131A, UL83; 5-238: gH, gL, UL128, UL130, UL131a; 5-239: gH, gL, UL128, UL130, UL83; 5-240: gH, gL, UL128, UL131A, UL83; 5-241: gH, gL, UL130, UL131A, UL83; 5-242: gH, gO, UL128, UL130, UL131a; 5-243: gH, gO, UL128, UL130, UL83; 5-244: gH, gO, UL128, UL131A, UL83; 5-245: gH, gO, UL130, UL131A, UL83; 5-246: gH, UL128, UL130, UL131A, UL83; 5-247: gL, gO, UL128, UL130, UL131a; 5-248: gL, gO, UL128, UL130, UL83; 5-249: gL, gO, UL128, UL131A, UL83; 5-250: gL, gO, UL130, UL131A, UL83; 5-251: gL, UL128, UL130, UL131A, UL83; and 5-252: gO, UL128, UL130, UL131A, UL83. In some embodiments, these vaccines comprise one or more of the coding sequences encoding each of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a that have sequences selected from the group consisting of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 and 60. In some embodiments, one or more of the coding sequences is selected from the group consisting of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 and 59. In some embodiments, one or more of the coding sequences in a vaccine is selected from the group consisting of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 and 59.

Example 8

In some embodiments, a composition comprising coding sequences for four of: gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83, or multiple compositions which collectively comprise coding sequences for four of: gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83 are administered. The composition may comprises coding sequences of four of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83, or combinations of compositions that collectively comprise coding sequences of four of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83. The following combinations 4-1 to 4-210 may be present in a four antigen vaccine: 4-1: gB, gM, gN, gH; 4-2: gB, gM, gN, gL; 4-3: gB, gM, gN, gO; 4-4: gB, gM, gN, U128; 4-5: gB, gM, gN, U130; 4-6: gB, gM, gN, U131a; 4-7: gB, gM, gN, U83; 4-8: gB, gM, gH, gL; 4-9: gB, gM, gH, gO; 4-10: gB, gM, gH, U128; 4-11: gB, gM, gH, U130; 4-12: gB, gM, gH, U131A; 4-13: gB, gM, gH, U83; 4-14: gB, gM, gL, gO; 4-15: gB, gM, gL, U128; 4-16: gB, gM, gL, U130; 4-17: gB, gM, gL, U131A; 4-18: gB, gM, gL, U83; 4-19: gB, gM, gO, U128; 4-20: gB, gM, gO, U130; 4-21: gB, gM, gO, U131A; 4-22: gB, gM, gO, U83; 4-23: gB, gM, U128; 4-24: gB, gM, U128; U131A; 4-25: gB, gM, U128; U83; 4-26: gB, gM, U130; U131A; 4-27: gB, gM, U130; U83; 4-28: gB, gM, U131A; U83; 4-29: gB, gN, gH, gL; 4-31: gB, gN, gH, gO; 4-32: gB, gN, gH, U128; 4-33: gB, gN, gH, U130; 4-34: gB, gN, gH, U131A; 4-35: gB, gN, gH, U83; 4-36: gB, gN, gL, gO; 4-37: gB, gN, gL, U128; 4-38: gB, gN, gL, U130; 4-39: gB, gN, gL, U131A; 4-40: gB, gN, gL, U83; 4-41: gB, gN, gO, U128; 4-42: gB, gN, gO, U130; 4-43: gB, gN, gO, U131A; 4-44: gB, gN, gO, U83; 4-45: gB, gN, U128; U130;

4-46: gB, gN, U128; U131A; 4-47: gB, gN, U128; U83; 4-48: gB, gN, U130; U131A; 4-49: gB, gN, U130; U83; 4-50: gB, gN, U131A; U83; 4-51: gB, gH, gL, gO; 4-52: gB, gH, gL, U128; 4-53: gB, gH, gL, U130; 4-54: gB, gH, gL, U131A; 4-55: gB, gH, gL, U83; 4-56: gB, gH, gO, U128; 4-57: gB, gH, gO, U130; 4-58: gB, gH, gO, U131A; 4-59: gB, gH, gO, U83; 4-60: gB, gH, U128; U130; 4-61: gB, gH, U128; U131A; 4-62: gB, gH, U128; U83; 4-63: gB, gH, U130; U131A; 4-64: gB, gH, U130; U83; 4-65: gB, gH, U131A; U83; 4-66: gB, gL, gO, U128; 4-67: gB, gL, gO, U130; 4-68: gB, gL, gO, U131A; 4-69: gB, gL, gO, U83; 4-70: gB, gL, U128; U130; 4-71: gB, gL, U128; U131A; 4-72: gB, gL, U128; U83; 4-73: gB, gL, U130; U131A; 4-74: gB, gL, U130; U83; 4-75: gB, gL, U131A; U83; 4-76: gB, gO, U128; U130; 4-77: gB, gO, U128; U131A; 4-78: gB, gO, U128; U83; 4-79: gB, gO, U130; U131A; 4-80: gB, gO, U130; U83; 4-81: gB, gO, U131A; U83; 4-82: gB, U128; U130; U131A; 4-83: gB, U128; U130; U83; 4-84: gB, U128; U131A; U83; 4-85: gB, U130; U131A; U83; 4-86: gM, gN, gH, gL; 4-87: gM, gN, gH, gO; 4-88: gM, gN, gH, U128; 4-89: gM, gN, gH, U130; 4-90: gM, gN, gH, U131A; 4-91: gM, gN, gH, U83; 4-92: gM, gN, gL, gO; 4-93: gM, gN, gL, U128; 4-94: gM, gN, gL, U130; 4-95: gM, gN, gL, U131A; 4-96: gM, gN, gL, U83; 4-97: gM, gN, gO, U128; 4-98: gM, gN, gO, U130; 4-99: gM, gN, gO, U131A; 4-100: gM, gN, gO, U83; 4-101: gM, gN, U128; U130; 4-102: gM, gN, U128; U131A; 4-103: gM, gN, U128; U83; 4-104: gM, gN, 0130; U131A; 4-105: gM, gN, 0130; U83; 4-106: gM, gN, U131A; U83; 4-107: gM, gH, gL, gO; 4-108: gM, gH, gL, U128; 4-109: gM, gH, gL, U130; 4-110: gM, gH, gL, U131A; 4-111: gM, gH, gL, U83; 4-112: gM, gH, gO, U128; 4-113: gM, gH, gO, U130; 4-114: gM, gH, gO, U131A; 4-115: gM, gH, gO, U83; 4-116: gM, gH, U128; U130; 4-117: gM, gH, U128; U131A; 4-118: gM, gH, U128; U83; 4-119: gM, gH, U130; U131A; 4-120: gM, gH, U130; U83; 4-121: gM, gH, U131A; U83; 4-122: gM, gL, gO, U128; 4-123: gM, gL, gO, U130; 4-124: gM, gL, gO, U131A; 4-125: gM, gL, gO, U83; 4-126: gM, gL, U128; U130; 4-127: gM, gL, U128; U131A; 4-128: gM, gL, U128; U83; 4-129: gM, gL, U130; U131A; 4-130: gM, gL, U130; U83; 4-131: gM, gL, U131A; U83; 4-132: gM, gO, U128; U130; 4-133: gM, gO, U128; U131A; 4-134: gM, gO, U128; U83; 4-135: gM, gO, U130; U131A; 4-136: gM, gO, U130; U83; 4-137: gM, gO, U131A; U83; 4-138: gM, U128; U130; U131A; 4-139: gM, U128; U130; U83; 4-140: gM, U128; U131A; U83; 4-141: gM, U130; U131A; U83; 4-142: gN, gH, gL, gO; 4-143: gN, gH, gL, U128; 4-144: gN, gH, gL, U130; 4-145: gN, gH, gL, U131A; 4-146: gN, gH, gL, U83; 4-147: gN, gH, gO, U128; 4-148: gN, gH, gO, U130; 4-149: gN, gH, gO, U131A; 4-150: gN, gH, gO, U83; 4-151: gN, gH, U128; U130; 4-152: gN, gH, U128; U131A; 4-153: gN, gH, U128; U83; 4-154: gN, gH, U130; U131A; 4-155: gN, gH, U130; U83; 4-156: gN, gH, U131A; U83; 4-157: gN, gL, gO, U128; 4-158: gN, gL, gO, U130; 4-159: gN, gL, gO, U131A; 4-160: gN, gL, gO, U83; 4-161: gN, gL, U128; U130; 4-162: gN, gL, U128; U131A; 4-163: gN, gL, U128; U83; 4-164: gN, gL, U130; U131A; 4-165: gN, gL, U130; U83; 4-166: gN, gL, U131A; U83; 4-167: gN, gO, U128; U130; 4-168: gN, gO, U128; U131A; 4-169: gN, gO, U128; U83; 4-170: gN, gO, U130; U131A; 4-171: gN, gO, U130; U83; 4-172: gN, gO, U131A; U83; 4-173: gN, U128; U130; U131A; 4-174: gN, U128; U130; U83; 4-175: gN, U128; U131A; U83; 4-176: gN, U130; U131A; U83; 4-177: gH, gL, gO, U128; 4-178: gH, gL, gO, U130; 4-179: gH, gL, gO, U131A; 4-180: gH, gL, gO, U83; 4-181: gH, gL, U128; U130; 4-182: gH, gL, U128; U131A; 4-183: gH, gL, U128; U83; 4-184: gH, gL, U130; U131A; 4-185: gH, gL, 0130;

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U83; 4-186: gH, gL, U131A; U83; 4-187: gH, gO, U128; U130; 4-188: gH, gO, U128; U131A; 4-189: gH, gO, U128; U83; 4-190: gH, gO, U130; U131A; 4-191: gH, gO, U130; U83; 4-192: gH, gO, U131A; U83; 4-193: gH, U128; U130; U131A; 4-194: gH, U128; U130; U83; 4-195: gH, U128; U131A; U83; 4-196: gH, U130; U131A; U83; 4-197: gL, gO, U128; U130; 4-198: gL, gO, U128; U131A; 4-199: gL, gO, U128; U83; 4-200: gL, gO, U130; U131A; 4-201: gL, gO, U130; U83; 4-202: gL, gO, U131A; U83; 4-202: gL, U128; U130; U131A; 4-203: gL, U128; U130; U83; 4-204: gL, U128; U131A; U83; 4-205: gL, U130; U131A; U83; 4-206: gO, U128; U130; U131A; 4-207: gO, U128; U130; U83; 4-208: gO, U128; U131A; U83; 4-209: gO, U130; U131A; U83; and 4-210: U128; U130; U131A; U83. In some embodiments, these vaccines comprise one or more of the coding sequences encoding each of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a that have sequences selected from the group consisting of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 and 60. In some embodiments, one or more of the coding sequences is selected from the group consisting of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 and 59. In some embodiments, one or more of the coding sequences in a vaccine is selected from the group consisting of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 and 59.

Example 9

In some embodiments, a composition comprising coding sequences for three of: gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83, or multiple compositions which collectively comprise coding sequences for three of: gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83 are administered. The composition which comprises coding sequences of three of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83, or combinations of compositions that collectively comprise coding sequences of three of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83 are referred to as "three antigen vaccines". The following combinations 3-1 to 3-120 may be present in a three antigen vaccine: 3-1: gB, gM, gN; 3-2: gB, gM, gH; 3-3: gB, gM, gL; 3-4: gB, gM, gO; 3-5: gB, gM, UL128; 3-6: gB, gM, UL130; 3-7: gB, gM, UL131A; 3-8: gB, gM, UL83; 3-9: gB, gN, gH; 3-10: gB, gN, gL; 3-11: gB, gN, gO; 3-12: gB, gN, UL128; 3-13: gB, gN, UL130; 3-14: gB, gN, UL131A; 3-15: gB, gN, UL83; 3-16: gB, gH, gL; 3-17: gB, gH, gO; 3-18: gB, gH, UL128; 3-19: gB, gH, UL130; 3-20: gB, gH, UL131A; 3-21: gB, gH, UL83; 3-22: gB, gL, gO; 3-23: gB, gL, UL128; 3-24: gB, gL, UL130; 3-25: gB, gL, UL131A; 3-26: gB, gL, UL83; 3-27: gB, gO, UL128; 3-28: gB, gO, UL130; 3-29: gB, gO, UL131A; 3-30: gB, gO, UL83; 3-31: gB, UL128, UL130; 3-32: gB, UL128, UL131A; 3-33: gB, UL128, UL83; 3-34: gB, UL130, UL131A; 3-35: gB, UL130, UL83; 3-36: gB, UL131A, UL83; 3-37: gM, gN, gH; 3-38: gM, gN, gL; 3-39: gM, gN, gO; 3-40: gM, gN, UL128; 3-41: gM, gN, UL130; 3-42: gM, gN, UL131A; 3-43: gM, gN, UL83; 3-44: gM, gH, gL; 3-45: gM, gH, gO; 3-46: gM, gH, UL128; 3-47: gM, gH, UL130; 3-48: gM, gH, UL131A; 3-49: gM, gH, UL83; 3-50: gM, gL, gO; 3-51: gM, gL, UL128; 3-52: gM, gL, UL130; 3-53: gM, gL, UL131A; 3-54: gM, gL, UL83; 3-55: gM, gO, UL128; 3-56: gM, gO, UL130; 3-57: gM, gO, UL131A; 3-58: gM, gO, UL83; 3-59: gM, UL128, UL130; 3-60: gM, UL128, UL131A; 3-61: gM, UL128, UL83; 3-62: gM, UL130, UL131A; 3-63: gM, UL130, UL83; 3-64: gM,

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UL131A, UL83; 3-65: gN, gH, gL; 3-66: gN, gH, gO; 3-67: gN, gH, UL128; 3-68: gN, gH, UL130; 3-69: gN, gH, UL131A; 3-70: gN, gH, UL83; 3-71: gN, gL, gO; 3-72: gN, gL, UL128; 3-73: gN, gL, UL130; 3-74: gN, gL, UL131A; 3-75: gN, gL, UL83; 3-76: gN, gO, UL128; 3-77: gN, gO, UL130; 3-78: gN, gO, UL131A; 3-79: gN, gO, UL83; 3-80: gN, UL128, UL130; 3-81: gN, UL128, UL131A; 3-82: gN, UL128, UL83; 3-83: gN, UL130, UL131A; 3-84: gN, UL130, UL83; 3-85: gN, UL131A, UL83; 3-86: gH, gL, gO; 3-87: gH, gL, UL128; 3-88: gH, gL, UL130; 3-89: gH, gL, UL131A; 3-90: gH, gL, UL83; 3-91: gH, gO, UL128; 3-92: gH, gO, UL130; 3-93: gH, gO, UL131A; 3-94: gH, gO, UL83; 3-95: gH, UL128, UL130; 3-96: gH, UL128, UL131A; 3-97: gH, UL128, UL83; 3-98: gH, UL130, UL131A; 3-99: gH, UL130, UL83; 3-100: gH, UL131A, UL83; 3-101: gL, gO, UL128; 3-102: gL, gO, UL130; 3-103: gL, gO, UL131A; 3-104: gL, gO, UL83; 3-105: gL, UL128, UL130; 3-106: gL, UL128, UL131A; 3-107: gL, UL128, UL83; 3-108: gL, UL130, UL131A; 3-109: gL, UL130, UL83; 3-110: gL, UL131A, UL83; 3-111: gO, UL128, UL130; 3-112: gO, UL128, UL131A; 3-113: gO, UL128, UL83; 3-114: gO, UL130, UL131A; 3-115: gO, UL130, UL83; 3-116: gO, UL131A, UL83; 3-117: UL128, UL130, UL131A; 3-118: UL128, UL130, UL83; 3-119: UL128, UL131A, UL83; and 3-120: UL130, UL131A, UL83. In some embodiments, these vaccines comprise one or more of the coding sequences encoding each of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a that have sequences selected from the group consisting of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 and 60. In some embodiments, one or more of the coding sequences is selected from the group consisting of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 and 59. In some embodiments, one or more of the coding sequences in a vaccine is selected from the group consisting of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 and 59.

Example 10

In some embodiments, a composition comprising coding sequences for two of: gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83, or multiple compositions which collectively comprise coding sequences for two of: gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83 are administered. The composition may comprises coding sequences of two of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83, or combinations of compositions that collectively comprise coding sequences of two of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, U83. There are 45 subsets (2-1 to 2-45) having 2 antigens from the set of HCMV antigens consisting of: gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a and UL83. The following combinations 2-1 to 2-45 may be present in a two antigen vaccine: 2-1 gB, gM, 2-2 gB, gN, 2-3 gB, gH, 2-4 gB, gL, 2-5 gB, gO, 2-6 gB, UL128, 2-7 gB, UL130, 2-8 gB, UL131a, 2-9 gB, UL83, 2-10 gM, gN, 2-11 gM, gH, 2-12 gM, gL, 2-13 gM, gO, 2-14 gM, UL128, 2-15 gM, UL130, 2-16 gM, UL131a, 2-17 gM, UL83, 2-18 gN, gH, 2-19 gN, gL, 2-20 gN, gO, 2-21 gN, UL128, 2-22 gN, UL130, 2-23 gN, UL131a, 2-24 gN, UL83 2-25 gH, gL, 2-26 gH, gO, 2-27 gH, UL128, 2-28 gH, UL130, 2-29 gH, UL131a, 2-30 gH, UL83 2-31 gL, gO, 2-32 gL, UL128, 2-33 gL, UL130, 2-34 gL, UL131a, 2-35 gL, UL83 2-36 gO, UL128, 2-37 gO, UL130, 2-38 gO, UL131a, 2-39 gO, UL83 2-40 UL128, UL130, 2-41 UL128,

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UL131a, 2-42 UL128, UL83 2-43 UL130, UL131a, 2-44 UL130, UL83, and 2-45 UL131a, UL83. In some embodiments, these vaccines comprise one or more of the coding sequences encoding each of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a that have sequences selected from the group consisting of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 and 60. In some embodiments, one or more of the coding sequences is selected from the group consisting of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 and 59. In some embodiments, one or more of the coding sequences in a vaccine is selected from the group consisting of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 and 59.

Example 11

In some embodiments, a composition comprising coding sequence for one of: gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a, and UL83 is administered. The following combinations 1-1 to 1-10 may be present in a one antigen vaccine: 1-1 gB, 1-2 gM, 1-3 gN, 1-4 gH, 1-5 gL, 1-6 gO, 1-7 UL128, 1-8 UL130, 1-9 UL131a and 1-10 U83. In some embodiments, these vaccines comprise one of the coding sequences encoding gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a that has a sequences selected from the group consisting of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 and 60. In some embodiments, the coding sequence is selected from the group consisting of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 and 59. In some embodiments, the coding sequences in a vaccine is selected from the group consisting of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57 and 59.

Example 12

In some embodiments, vaccines comprise coding sequences encoding coding sequences for one, two, three, four, five, six, seven, eight, nine or ten antigens selected from the group consisting of each of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a. In some embodiments, vaccines comprise coding sequences encoding coding sequences for one, two, three, four, five, six, seven, eight, nine or ten antigens selected from the group consisting of each of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a wherein one or more of said sequences is selected from the group consisting of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 and 60. In some embodiments, vaccines comprise coding sequences encoding coding sequences for one, two, three, four, five, six, seven, eight, nine or ten antigens selected from the group consisting of each of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a wherein two or more of said sequences is selected from the group consisting of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 and 60. In some embodiments, vaccines comprise coding sequences encoding coding sequences for one, two, three, four, five, six, seven, eight, nine or ten antigens selected from the group consisting of each of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a wherein three or more of said sequences is selected from the group consisting of

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SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 and 60. In some embodiments, vaccines comprise coding sequences encoding coding sequences for one, two, three, four, five, six, seven, eight, nine or ten antigens selected from the group consisting of each of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a wherein four or more of said sequences is selected from the group consisting of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 and 60. In some embodiments, vaccines comprise coding sequences encoding coding sequences for one, two, three, four, five, six, seven, eight, nine or ten antigens selected from the group consisting of each of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a wherein five or more of said sequences is selected from the group consisting of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 and 60. In some embodiments, vaccines comprise coding sequences encoding coding sequences for one, two, three, four, five, six, seven, eight, nine or ten antigens selected from the group consisting of each of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a wherein six or more of said sequences is selected from the group consisting of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 and 60. In some embodiments, vaccines comprise coding sequences encoding coding sequences for one, two, three, four, five, six, seven, eight, nine or ten antigens selected from the group consisting of each of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a wherein seven or more of said sequences is selected from the group consisting of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 and 60. In some embodiments, vaccines comprise coding sequences encoding coding sequences for one, two, three, four, five, six, seven, eight, nine or ten antigens selected from the group consisting of each of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a wherein eight or more of said sequences is selected from the group consisting of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 and 60. In some embodiments, vaccines comprise coding sequences encoding coding sequences for one, two, three, four, five, six, seven, eight, nine or ten antigens selected from the group consisting of each of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a wherein nine or more of said sequences is selected from the group consisting of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 and 60. In some embodiments, vaccines comprise coding sequences encoding coding sequences for one, two, three, four, five, six, seven, eight, nine or ten antigens selected from the group consisting of each of gB, gM, gN, gH, gL, gO, UL128, UL130, UL131a wherein ten or more of said sequences is selected from the group consisting of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58 and 60.

Example 13

HCMV Antigen Expression

Following construction, protein expression was confirmed by immunoblotting. 293T cells were transfected with each plasmid or empty pVAX vector (negative control) and samples were harvested 48 h later and analyzed by Western immunoblotting (photo not shown). The presence of a ~66 kDa protein was detected in the cell lysates of pHCMV-NP-

transfected 293T cells using anti-HA tag Abs (data not shown) and NP-specific polyclonal serum (data not shown), while control pVAX empty vector-transfected lysates were negative for Ag expression. Samples were normalized for total protein by Bradford protein assay and contained equivalent amounts of globular tubulin protein. Furthermore, pHCMV-NP-transfected 293T cells were reactive with serum from HCMV immune and pHCMV-NP immunized mice (n=5), but not from pVAX immunized (n=5) animals (data not shown); hyper-immune serum pooled from mice immunized five times with pHCMV-NP reacted with 16.6% of pHCMV-NP-transfected cells on average as compared with 8.1% from HCMV immune animals and 0.7% from pVAX-transfected mice (data not shown). Non-specific binding was not detected as the positive sera did not react with pVAX-transfected 293T cells. Furthermore, Western immunoblotting confirmed host-cell proteolytic cleavage of the three fusion proteins segregated by Turin cleavage sites into independent Ags gM, gN, gH, gL, UL128, UL130, and UL131A.

Western Blot Analysis

Expression of the plasmid DNA-encoded vaccine proteins was verified by Western immunoblotting. 293T cells (1×10^6 cells) were transfected using the Fugene transfection method (Roche, Indianapolis, Ind.). Forty-eight hours post-transfection, proteins were isolated using cell lysis buffer, fractionated on SDS-PAGE (12%), and transferred to nitrocellulose using iBlot Dry Blotting System (Invitrogen, CA, USA). Immunodetection was performed using SNAP i.d. Protein Detection System (Millipore, Mass., USA) with specific mouse antiserum (pooled from individual groups of mice immunized 4-6 times using the respective plasmid DNA construct) and the expressed proteins were visualized with horseradish peroxidase-conjugated goat anti-mouse IgG using an ECL detection system (Amersham Pharmacia Biotech, Piscataway, N.J.).

Altogether, transfection of 293T cells using the each of the plasmid DNA constructs was sufficient for the production of the consensus immunogens in vitro that was specifically reactive with Abs generated from repeat immunization of mice.

Epitope Mapping

Data was generated to identify immunodominant epitopes of HCMV-gB using splenocytes from animal vaccinated with plasmid 1 and a series of overlapping peptides of HCMV-gB. ELISpot data is shown in FIG. 10.

Data was generated to identify immunodominant epitopes of HCMV-gH and HCMV-gL using splenocytes from animal vaccinated with plasmid 3 and a series of overlapping peptides of HCMV-gH and HCMV-gL. ELISpot data is shown in FIG. 11.

Data was generated to identify immunodominant epitopes of HCMV-gM and HCMV-gN using splenocytes from animal vaccinated with plasmid 2 and a series of overlapping peptides of HCMV-gM and HCMV-gN. Data was generated to identify immunodominant epitopes of HCMV-gO using splenocytes from animal vaccinated with plasmid 4 and a series of overlapping peptides of HCMV-gO. ELISpot data is shown in FIG. 12.

Data was generated to identify immunodominant epitopes of HCMV-UL131A, HCMV-UL130 and HCMV-UL128 using splenocytes from animal vaccinated with plasmid 5 and a series of overlapping peptides of HCMV-UL131A, HCMV-UL130 and HCMV-UL128. Data was generated to identify immunodominant epitopes of HCMV-UL83 using

splenocytes from animal vaccinated with plasmid 6 and a series of overlapping peptides of HCMV-UL83. ELISpot data is shown in FIG. 13.

See also FIG. 18a for epitope analysis.

Example 14

HCMV Plasmid Immunization and Mice

Adult female C57BL/6 (H-2^b) mice 6-8 weeks of age were purchased from The Jackson Laboratory (Bar Harbor, Me.) and were cared for in accordance with Institutional Animal Care and Use Committee-approved protocols at the University Pennsylvania School of Medicine Animal Facility. Mice were immunized with the indicated doses of plasmid DNA by i.m. injection into the anterior tibialis muscle followed by in vivo electroporation (EP) using the CELLECTRA® adaptive constant current EP Minimally Invasive Device (MID) (Inovio Pharmaceuticals, Blue Bell, Pa.) as described previously [Khan, 2005 #727; Shedlock, 2011 #1097]. A total of four 0.1 Amp constant current square-wave pulses were delivered as two sets of two pulses through a triangular 3-electrode array consisting of 26-gauge solid stainless steel electrodes. Each pulse was 52 milliseconds in length with a 1 second delay between the individual pulses with three seconds between the sets of pulses.

The native, virus-derived DNA sequence of the HCMV NP protein ('Native' or non-optimized) was compared with a gene that was optimized for its host species for immunogenicity in the DNA vaccination of mice (FIG. 16a). Mice (n=10) were immunized twice with 35 µg of either the 'Native' or 'Optimized' gene subcloned into a modified mammalian DNA expression vector and delivered with EP, and T cell immunity was assessed 8 days later. NP-specific T cells were 2-fold greater (p=0.0001) in mice immunized with the 'Optimized' construct thus demonstrating that species-specific gene optimization can enhance DNA vaccine-induced T cell immunity.

The contribution of in vivo EP delivery to the elicitation of T and B cell immunity was also assessed. The 'Optimized' version of the HCMV NP DNA vaccine was administered to mice (n=5-10/group) similarly as above, but delivered either with or without EP, and protective efficacy was assessed with lethal challenge (FIG. 16b). While both vaccines elicited protective efficacy when compared with the control vector, EP delivery during DNA vaccination was completely protective versus only 60% protection without. These data show a significant contribution by EP delivery to the generation of T cells that mediate protective efficacy against lethal challenge. For evaluation of EP contribution to the generation of B cells, animals were immunized (n=5/group) several times and Ab production was compared 7 days after each injection with that from wild type HCMV infection (FIG. 16c). While animals immunized with DNA alone yielded NP-specific Abs only after a total of 4 immunizations, those that received vaccine delivered with EP exhibited Abs after the second administration. Furthermore, Ab responses in the EP-immunized mice surpassed those in mice following wild type HCMV infection, which demonstrated that EP delivery is a potent technology for enhancing DNA vaccine-induced immunity.

DNA Vaccination Induces Robust T and B Cell Immunity

A summary of DNA vaccine data is shown in FIG. 15. These data show that highly effective immune responses induced by vaccines exemplified herein were observed. The HCMV-gHgL data show the construct as an outstanding vaccine target with superior efficacy, providing high neutralizing titers and CTL epitopes. Such a construct can be

delivered as a DNA vaccine or used as a component of other vaccine platforms. Similarly, the HCMV: UL131A, UL130, and UL138 complex immunogen possesses both CTL activity as well as neutralization activity supporting its importance as a novel vaccine target. The data also shows that the designed HCV-gMgN is established for vaccine production, that HCMV-gO is established for protection and that the importance of multiantigen approach is established as a viable example.

For evaluation of plasmid DNA immunogenicity, mice (n=4-6/group) were immunized twice with 45 µg of each respective plasmid vaccine, two weeks between injections and immediately followed by EP. Mice were sacrificed 7-8 days following the second immunization and ELISPOT and FACS was performed to assess T cell immunity. Immunization with the novel gHgL vaccine resulted in the highest level of T cell immunity (~>10,000 IFN γ -producing cells per million splenocytes) followed by pUL (~8,000 cells). Moreover, the breadth of the epitopic responses for each vaccine was assessed and showed that DNA vaccination with a combination of optimization strategies generated a diversity of T cell epitopes. Altogether, these data show that all six HCMV DNA vaccine constructs were immunogenic in mice following immunization in combination with in vivo EP and yielded measurable immunogen-specific T cell responses; and T cell immunogenicity was ranked as follows: gHgL>pUL>UL83>gB>gMgN>gO (see FIGS. 18b-d).

Serum samples were collected and pooled from each group of mice (n=5) 7-10 days following each of five to six immunizations (spaced two weeks apart), and then pooled thereafter up to 1 month following the final immunization. Furthermore, serum was collected 6 months following each of the final immunizations (a time point considered to be clinically relevant for long-term Ab responses) and tested along with the pooled-effector sera for the capacity for neutralization of infection with the AD169-EGFP virus into life extended human foreskin fibroblast cells. Data confirmed a neutralization capacity for gB immunized animals which supports previous data demonstrating its ability to elicit nAbs and protect in some challenge models. See FIGS. 19a-b. However, immunization with the novel gHgL DNA vaccine generated nAb responses that were ~2-4-fold greater than gB immunization. Interestingly, neither of these levels of neutralization ability was achieved by any other immunogen, including the gMgN, gO, UL128-131A, nor the UL83. However, this is not entirely unexpected for the UL128-131A plasmid since the AD169 vector is known to contain a sizable mutation/deletion in the 131A protein. Lastly, neutralization levels were relatively stable for each immunogen comparing effector and memory serum collected 6 months following the final immunization. Thus, these data demonstrate that DNA vaccination in combination with EP generated robust B cell responses. Altogether, data herein show that the DNA plasmids were immunogenic in mice and generated robust T and B cell responses.

Immunity to the HCMV gB alone has been demonstrated to completely protective in guinea pigs, but has limited efficacy in the clinic. Thus, we next set out to determine whether their combination with the gB DNA vaccine would enhance HCMV-specific immunity. Mice (n=5/group) were given several doses of the gB plasmid alone, gB+gHgL, or gB+gHgL+pUL, and T and B cell immunity was assessed. Indeed, trivalent formulation of these plasmids induced the highest level of both T and B cell responses. Thus, these data demonstrate that vaccine-induced CMV-specific immunity can be increased by immunization with multi-valent plasmid DNA formulations.

Sero-Reactivity to gH/gL Correlates with Virus Neutralization

FIG. 19 shows graphs that neutralization data for: a) 50% neutralization levels for HCMV: gB, gMgN, gHgL, gO, UL, and UL83, and b) 50% neutralization levels for CMV only, seropositive serum, and HCMV-gHgL immunized serum. Splenocyte Isolation and ELISpot Assay

Mice were sacrificed 8 days following the final immunization with plasmid DNA and the spleens were harvested and placed in RPMI 1640 medium (Mediatech Inc., Manassas, Va.) supplemented with 10% FBS, 1 \times Anti-anti (Invitrogen), and 1 \times β -ME (Invitrogen). Splenocytes were isolated by mechanical disruption of the spleen using a Stomacher machine (Seward Laboratory Systems Inc., Bohemia, N.Y.), and the resulting product was filtered using a 40 µm cell strainer (BD Falcon). The cells were treated for 5 min with ACK lysis buffer (Lonza, Switzerland) for lysis of RBCs and then the splenocytes were washed in PBS and then resuspended in complete RPMI medium.

An IFN γ ELISPOT assay was conducted. Briefly, ELISPOT 96-well plates (Millipore, Billerica, Mass.) were coated with anti-mouse IFN- γ capture antibody and incubated for 24 h at 4° C. (R&D Systems, Minneapolis, Minn.). The following day, plates were washed with PBS and then blocked for 2 h with blocking buffer (1% BSA and 5% sucrose in PBS). One to two-hundred thousand splenocytes per well and in triplicate from each animal were stimulated overnight at 37° C. in 5% CO $_2$ and in the presence of RPMI 1640 (negative control), Concanavalin A (Con A; positive control), or with individual (individual peptides overlapping complete vaccine proteins were used for the Single Peptide Analysis (SPA) as indicated) or pooled 15-mer peptides as indicated (GenScript). After approximately 18-20 h of stimulation, the cells were washed in PBS and incubated for 24 h at 4° C. with biotinylated anti-mouse IFN- γ mAb (R&D Systems, Minneapolis, Minn.). The plates were washed in PBS, and streptavidin-alkaline phosphatase (MabTech, Sweden) was added to each well and incubated for 2 h at room temperature. The plates were washed again in PBS, BCIP/NBT Plus substrate (MabTech) was added to each well for 15-30 min, and then the plate was rinsed with distilled water and dried at room temperature. Spots were counted with an automated ELISPOT reader (Cellular Technology Ltd., Shaker Heights, Ohio).

Moreover, splenocytes from immunized mice were stimulated with individual peptides (15-mers overlapping by 11 amino acids and spanning the entire lengths of their respective DNA vaccine-encoded Ags) to also assess the breadth of the epitopic response and data are displayed in FIGS. 10-13 and FIG. 18a. To better visualize positive T-cell responses for the identification of epitope-containing peptides, ELISPOT data from each animal were stacked in bar graph form and expressed as the SUM of the IFN γ + response per group. Epitope-comprising peptides were considered positive only if they stimulated at least 10 spots on average with an 80% or higher response rate.

Immunization with any of the six HCMV DNA plasmid vaccines were observed to stimulated a diversity of measurable T-cell epitopes; HCMV-gB induced X epitopes, HCMV-gMgN-X, HCMV-gHgL-X, HCMV-gO-C, HCMV-pUL-X, and HCMV-UL83-X. Additionally, immunodominant epitopes were observed in all mice (#5:GP $_{25-39}$ in H-2 b mice and #27:GP $_{151-171}$ in H-2 d mice) and pEBOZ (#4:GP $_{19-33}$ in H-2 b mice and #41:GP $_{241-255}$ in H-2 d mice), while pEBOZ stimulated them only in the H-2 d mice (#24: $_{139-153}$, #30: $_{175-189}$, and #66: $_{391-405}$). See FIGS. 10-13 and FIG. 18a. Moreover, data for epitope-containing pep-

tides are further characterized in Table 1 in which predicted epitope sequences are displayed and T cell responses were confirmed and de-convoluted by flow cytometry. Total DNA

vaccine-induced IFN γ + responses are reported and are the SUM of the average responses per positively identified epitope—see Table 1 (below)

TABLE 1

Plasmid	CMV	α PEP	Best con. % rank (H-2 ^b)									
			ELISPOT		FACS	CD8+	(s0.6)	CD4+ (S28)				
Vaccine	ag	#	AA#	Peptide Sequence	AVE	\pm SEM	T cell	Db	Kb	I-ab		
pHCMV-gB	gB	5	25-39	SSSTRGTSATHSHHS	388	140	8+			14.6		
		7	37-51	HHSSTTTAAHSRSG	37	35	4+			18.4		
		26	151-165	RRSYAYIHTTYLLGS	1,105	472	8+	0.1	0.2	13.5		
		28	163-177	LGSNTEYVAPPMWEI	30	16	4+			4.0		
		51	361-375	AEDSYVHFSSAKMTAT	577	430	4+		0.1	1.2		
		70	415-429	KYGNVSVFETTGGLV	183	89	8+		0.4			
		73*	433-447	QKIKQKSLVLELERLA	95	73	8+					
		74	439-453	SLVLELERLANRSSLN	360	146	8+					
		80	475-489	SVHNLVYAQLQFTYD	1,045	169	8+		0.2			
		88	523-537	INPSAILSATYKPI	53	31	4+			20.7		
		89	529-543	LSAIYINKPIAARFMG	18	13	4+	0.3		2.5		
		pHCMV-gHgL	gH	8	43-57	LNTYGRPIRFLRENT	38	33	8+			
				9	49-63	PIRFLRENTTQCTYN	26	15	4+			
11	61-75			TYNSSLRNSTVVREN	776	141	8+	0.1		24.5		
12	67-81			RNSTVRENATSFNF	72	46	8+					
13	73-87			RENALSFNFQSYNQ	94	28	8+	0.1	0.1			
15	85-99			YNQYVVFHMPRCLFA	559	231	4+			3.5		
16	91-105			FHMPCRCLFAGPLAEQ	419	199	4+			6.9		
17	97-111			LFAGPLAEQFLNQVD	261	139	4+			25.5		
20	115-129			TLERYQQRNLNTYALV	153	36	8+	0.6				
28	163-177			SIPHVWMPPTPHG	20	5	4+			1.2		
30	175-189			PHGWKESHTTSLGHR	2,942	81	8+			25.0		
42	247-261			MLLIPGHLPRVLFKA	78	58	4+	0.6	0.3	27.6		
43	253-267			HLPRVLFKAPYQRDN	24	9	4+			26.8		
50	295-309			DPDFLDAALDFNYLD	331	187	8+/4+		0.5			
51*	301-315			AALDFNYLDLSALLR	307	181	8+		0.5	16.1		
57	337-351			RTVEMAFAYALALFA	340	190	4+		0.4	1.6		
58	343-357			FAYALALFAAARQEE	265	157	4+	0.4		5.2		
59	349-363			LFAAARQEEAGAEVS	27	17	8+			12.9		
82	487-501			EIFIVETGLCSLAEI	64	31	4+					
90	535-549			RLTRLFPDATVPATV	81	32	8+			6.5		
97	577-591			ESFSALTVSEHVSIV	51	21	4+			15.9		
98*	583-597			TVSEHVSIVVTNQYL	10	5	8+					
99	589-603	SYVVTNQYLKGISY	17	4	8+	0.1						
110*	655-669	LLEYDDTQGVINIMY	191	83	8+							
111	661-675	TQGVINIMYMHDSDD	2,864	136	8+	0.4						
115	685-699	EVVSSPRTHYLMLL	22	14	4+			13.1				
117	697-711	MLLKNGTVLEVTDVV	58	23	4+	0.4						
120	715-729	TDSRLMMSVYALSA	14	4	4+							
121	721-735	MMSVYALSAIIGIYL	32	16	8+			7.4				
122	727-741	LSAIIIGIYLLYRMLK	13	9	8+	0.5	0.2					
	gL	9	49-63	ELTRRCLLGEVFQGD	25	15	4+					
		11	61-75	QGDKYESWLRPLVNV	76	41	4+			17.4		
		12	67-81	SWLRPLVNVTRDGP	128	64	4+					
		15	85-99	LIRYRPVTPEAANSV	483	220	4+			0.1		
		17	97-111	NSVLLDEAFDLTLAL	16	11	4+					
		19	109-123	LALLYNNPDQLRALL	186	87	4+			19.8		
		45	265-279	PAHSRYGPQAVDAR	41	24	4+			14.2		
pHCMV-UL83	UL83	14	79-93	HTYFTGSEVENSVSN	130	74	4+			11.4		
		16	91-105	SVNVHNPTRGSIKPS	106	46	8+/4+					
		17	97-111	PTGRSICPSQEFMSI	161	127	8+	0.6				
		18*	103-117	CPSQEFMSIYYVALP	39	28	8+		0.3			
		19	109-123	MSIYVVALPLKMLNI	427	196	4+	0.3	0.1			
		21	121-135	LNIPSIINVHHYPSAA	192	132	4+			16.9		
		22	127-141	NVHHYPSAAERKHRH	277	178	4+			15.2		
		29	169-183	TRQQNQWKEPDVYYT	192	115	4+					
		30	175-189	WKEPDVYYTSAFVFP	216	117	4+		0.6	23.1		
		31	181-195	YYTEAFVFPKDVVAL	338	161	8+/4+	0.6	0.5	4.8		
		38	223-237	YVKVYLESFCEDVPS	87	50	4+					
		39	229-243	ESFCEDVPSGKLFMH	117	62	4+					
		43	253-267	DLTMTRNPOPEMRPH	994	468	8+	0.5				
		44*	259-273	NPQPFRPHERNGFT	190	177	8+					
45	265-279	RPHERNGFTVLCPKN	150	97	8+							
51	301-315	HFGLLCFKSIPGLSI	45	22	4+			27.0				
55	325-339	QIFLEVQAIRETVEL	34	8	4+							

TABLE 1-continued

Plasmid	CMV	^a PEP		Peptide Sequence	ELISPOT		FACS	Best con. % rank (H-2 ^b)						
					AVE	±SEM		CD8+	(±0.6)	CD4+ (S28)				
Vaccine	ag	#	AA#				T cell	Db	Kb	I-ab				
pHCMV- UL	UL128	7	37-51	NHPPERCYDFKMCNR	172	107	8+							
		8*	43-57	CYDFKMCNRFVVALR	12	5	8+	0.1						
		13	73-87	IRGIVTMTTHSLTRQ	350	199	8+							
		16	91-105	NKLTSCNYPNPLYLEA	1,650	230	8+	0.2	0.2					
		17*	97-111	NYNPLYLEADGRIRC	454	58	8+							
		18	103-117	LEADGRIRCQKVNNDK	443	163	8+							
		19	109-123	IRCGKVNNDKAQYLLG	303	133	8+							
		20	115-129	NDKAQYLLGAAGSVP	100	52	4+			9.7				
		21*	121-135	LLGAAGSVPYRWINL	731	208	8+		0.2	24.4				
		22	127-141	SVPYRWINLEYDKIT	739	202	8+		0.2					
		23*	133-147	INLEYDKITRIVGLD	65	36	8+							
		24	139-153	KITRIVGLDQYLESV	89	50	8+							
		25	145-159	GLDQYLESVKKHKRL	56	32	8+							
		26	151-165	ESVKKHKRLDVCRAK	11	4	8+							
		28	163-171	RAKMGYMLQ	498	206	8+							
			UL130	3	13-27	LLLCVAVWATPCLASP	332	146	8+/4+			4.6		
				4	19-33	WATPCLASPWSTLTA	104	33	8+/4+			22.9		
				8	43-57	KLTYSKPHDAATFYC	465	169	8+/4+			15.1		
				9*	49-63	PHDAATFYCFPLYPS	237	185	8+/4+	0.2				
				10	55-69	FYCFPLYPSPPRSPL	222	179	8+/4+	0.6		0.6		
					UL131A	5	25-39	AEKNDYYRVPHYWDA	61	34	4+			
						6	31-45	YRVPHYWDACSRALP	223	130	4+			16.2
						11	61-75	LNHYHDASHGLDNFD	429	220	4+			12.1
						20	115-129	PHARSLLEFSVRLFAN	255	145	8+		0.6	
				pHCMV- gMgN	gM	4	19-33	VFMVLTFVNYSVHLV	153	39	8+		0.2	22.2
		6	31-46			HLVLSNFPFLGYPCV	31	7	8+	0.5	0.4	21.7		
		13	73-87			DSVQLVCYAVFMQLV	22	8	8+					
		17	97-111			VCWIKISMRKDKGMS	23	11	8+	0.3				
18*	103-117	SMRKDKGMSLNQSTR	15			3	8+							
26*	151-165	GMIAFMAAVHFFCLT	14			4	8+		0.3	26.2				
27	157-171	AAVHFFCLTIENVSM	21			10	8+	0.1						
30	175-189	YRSYKRSLEFFSRLH	258			93	8+	0.1	0.1					
31*	181-196	SLFFFSRLHPPKLGKT	57			8	8+	0.1	0.1	24.4				
33	193-207	KGTVQFRTLIVLNLE	14			8	4+		0.3	17.7				
34	199-213	RTLIVNLVEVALGFN	28			12	8+	0.4						
39	229-243	FFVRTFHMVLAVPV	32			15	8+							
49	289-303	TFLSNEYRTFISWSF	83			38	8+/4+							
50	295-309	YRTGISWSFGMLFFI	627			441	8+	0.1	0.1					
	gN	1	1-15			MEWNTLVGLLVLSV	472	343	8+					
		4	19-33			SNNTSTASTPSPSSS	33	11	4+			2.7		
		5	25-30			ASTPSPSSSTHTSTT	67	36	4+			16.0		
		12	67-81			STTHDPNVMRPHAHN	46	14	4+			25.0		
		13	73-87			NVMRPHAHNDFYKAH	182	48	4+					
		21	121-135			RHCCFQNFATTTKG	24	10	8+			8.6		
pHCMV- gO	gO	5	25-39	LLSLINCNVLVNSKG	65	47	8+	0.1						
		48	283-297	PYLSYTTSTAFNVTT	101	65	4+			2.4				
		51	301-315	YSATAAVTRVATSTT	43	8	4+			12.9				
		55	325-339	KSIMATQLRDLATWV	14	10	8+							
		56	331-345	QLRDLATWVYTTLRY	784	317	8+		0.2					
		57*	337-351	TWVYTTLRYRNEPFC	394	156	8+							

^a Epitope-containing peptides were identified by IFN γ ELISPOT (≥ 10 spots AND $\geq 80\%$ response rate)

All peptides identified by ELISPOT were confirmed by FACS ($\geq 3-5 \times 10^4$ CD3+ cells were acquired)

Responding T cells for each epitope-containing peptide were characterized by FACS (expression of CD4 and/or CD8 by CD3+/CD44+/IFN γ + cells).

Predicted CD8+ epitopes are underlined (best consensus % rank by IEDE) Contiguous peptide with shared and/or partial epitope as confirmed by ELISPOT (*)

No H-2b epitopes reported herein have been described (IEBS 70% BLAST)

Regarding fragment of HCMV antigens, preferably the fragments will have the following domains for each of the following HCMV antigens:

HCMV-gB: amino acid region 25-39 (peptide #5); amino acid region 151-165 (peptide #26); amino acid region 151-165 (peptide #26); amino acid region 361-375 (peptide #5=61); amino acid region 439-453 (peptide #74); and/or amino acid region 475-489 (peptide #80);

HCMV-gH: amino acid region 61-75 (peptide #11); amino acid region 85-99 (peptide #15); amino acid region 91-105 (peptide #15); amino acid region 175-189 (peptide #30); amino acid region 661-675 (peptide #111);

HCMV-gL: amino acid region 85-99 (peptide #15); HCMV-UL83: amino acid region 109-123 (peptide #19); amino acid region 253-267 (peptide #43);

HCMV-UL128: amino acid region 91-105 (peptide #16); amino acid region 97-111 (peptide #17); amino acid region

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103-117 (peptide #18); amino acid region 121-135 (peptide #21); amino acid region 127-141 (peptide #22); amino acid region 163-171 (peptide #28);

HCMV-UL130: amino acid region 13-27 (peptide #3); amino acid region 43-57 (peptide #8);

HCMV-UL131A: amino acid region 61-75 (peptide #11);

HCMV-gM: amino acid region 175-189 (peptide #30);

amino acid region 295-309 (peptide #50);

HCMV-gN: amino acid region 1-15 (peptide #1); and

HCMV-gO: amino acid region 331-345 (peptide #56); amino acid region 337-351 (peptide #57).

ELISA

To determine sera Ab titers against HCMV gB, gH or gL, Nunc-Immuno MaxiSorp plates (Nunc, Rochester, N.Y.) were coated overnight at 4° C. with recombinant protein (GenScript) at the indicated amounts or BSA (control) diluted in PBS. The next day, plates were washed with PBS, 0.05% Tween 20 (PBS-T), blocked for 1 h with 10% BSA/PBS-T, and incubated overnight at 4° C. with serial dilutions of serum from either human patients or immunized animals. Plates were then washed six times and bound IgG was detected using either goat anti-human IgG (Southern Biotech) or goat-anti mouse IgG (Santa Cruz, Santa Cruz, Calif.), both at a dilution of 1:5,000. Bound enzyme was detected by SigmaFAST™ O-phenylenediamine dihydrochloride (OPD; Sigma-Aldrich), and the optical density was determined at 450 nm on a Biotek (Winooski, Vt.) EL312e reader. The reciprocal endpoint titer was reported as the 10% of maximum OD calculated by curve fitting using the sigmoidal dose-response model with a variable slope in GraphPad Prism (GraphPad Software Inc., La Jolla, Calif.). Neutralization Assay

Serum samples were collected and pooled from each group of mice (n=5) 7-10 days following each of five to six immunizations (spaced two weeks apart), and then pooled thereafter up to 1 month following the final immunization. Furthermore, serum was collected 6 months following each of the final immunizations (a time point considered to be clinically relevant for long-term Ab responses) and tested along with the pooled-effector sera for the capacity for neutralization of infection with the relevant. Data confirmed a neutralization capacity for gB immunized animals which supports previous data demonstrating its ability to elicit nAbs and protect in some challenge models. However, immunization with the novel gHgL DNA vaccine generated nAb responses that were ~2-4-fold greater than gB immunization. Neutralizing antibody titers were measured using mouse serum from mice immunized with HCMV proteins and life-extended HFF (human foreskin fibroblasts) cells. The data is expressed as a geometric mean of 3 values with 95% CI. The data are shown in FIG. 14.

Interestingly, neither of these levels of neutralization ability was achieved by any other immunogen, including the gMgN, gO, UL128-131A, nor the UL83. Lastly, neutralization levels were relatively stable for each immunogen comparing effector and memory serum collected 6 months following the final immunization. Thus, these data demonstrate that DNA vaccination in combination with EP generated robust B cell responses. Altogether, data herein show that the DNA plasmids were immunogenic in mice and generated robust T and B cell responses.

Immunity to the HCMV gB alone has been demonstrated to completely protective in guinea pigs, but has limited efficacy in the clinic. Thus, we next set out to determine whether their combination with the gB DNA vaccine would enhance HCMV-specific immunity. Mice (n=5/group) were given several doses of the gB plasmid alone, gB+gHgL, or

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gB+gHgL+pUL, and T and B cell immunity was assessed. Indeed, trivalent formulation of these plasmids induced the highest level of both T and B cell responses. Thus, these data demonstrate that vaccine-induced CMV-specific immunity can be increased by immunization with multi-valent plasmid DNA formulations.

Example 15 a) HSV1 Antigen and Expression in 293T Cells

Using the same strategy as provided in Example 1, above, and the above example related to HCMV, HSV1 antigens were selected and nucleic acid constructs were made. HSV1 antigens selected based on the foregoing are: gB, gH, gL, gC, and gD. Furthermore, combinations as discussed herein were made, including HSV1-gHgL and HSV1-gCgD.

HSV1 gB, gC, and gD were found to be expressed on the surface of transfected cells, showing effective translation, translocation, presentation by cell; moreover, the combined antigens gCgD were found to co-express (data not shown). This was evidenced by MHC class I binding with the aforementioned antigens in serum (1:200 dilution) of animals immunized with the antigens, versus no antigen binding with serum from control (vector only).

Immuization with the same plasmids, above, was found to induce robust antibodies in vivo (data not shown).

b) HSV2 Antigen Expression in 293T Cells

Using the same strategy as provided in Example 1, above, and the above example related to HCMV, HSV2 antigens were selected and nucleic acid constructs were made. HSV2 antigens selected based on the foregoing are: gB, gH, gL, gC, and gD. Furthermore, combinations as discussed herein were made, including HSV2-gHgL and HSV2-gCgD.

HSV2 gB, gC, gD, gH and gL were found to be expressed on the surface of transfected cells, showing effective translation, translocation, presentation by cell; moreover, the combined antigens gCgD and gHgL were found to co-express (data not shown). This was evidenced by MHC class I binding with the aforementioned antigens in serum (1:200 dilution) of animals immunized with the antigens, versus no antigen binding with serum from control (vector only).

c) CeHV1 Antigen Expression in 293T Cells

Using the same strategy as provided in Example 1, above, and the above example related to HCMV, CeHV1 antigens were selected and nucleic acid constructs were made. CeHV1 antigens selected based on the foregoing are: gB, gH, gL, gC, and gD. Furthermore, combinations as discussed herein were made, including CeHV1-gHgL and CeHV1-gCgD.

CeHV1 gB, gC, and gD were found to be expressed on the surface of transfected cells, showing effective translation, translocation, presentation by cell; moreover, the combined antigens gCgD were found to co-express (data not shown). This was evidenced by MHC class I binding with the aforementioned antigens in serum (1:200 dilution) of animals immunized with the antigens, versus no antigen binding with serum from control (vector only).

Immuization with the same plasmids, above, was found to induce robust antibodies in vivo (data not shown).

d) VZV Antigen Expression in 293T Cells

Using the same strategy as provided in Example 1, above, and the above example related to HCMV, VZV antigens

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Gln Lys Val Leu Thr Phe Arg Arg Ser Tyr Ala Tyr Ile His Thr Thr
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Ile His His Ile Asn Ser His Ser Gln Cys Tyr Ser Ser Tyr Ser Arg
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Asn Lys Thr Met Gln Leu Met Pro Asp Asp Tyr Ser Asn Thr His Ser
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 aacgacttct acaaggccca ctgcaccagc catatgtacg agctgagcct gagcagcttc 300
 gccgcctggt ggaccatgct gaacgcccctg atcctgatgg ggcgcttctg catcggtgctg 360
 cggcactgct gcttccagaa cttcaccgcc acaaccacca agggctactg a 411

<210> SEQ ID NO 6
 <211> LENGTH: 136
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: gN consensus amino acid sequence
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 6

Xaa Glu Trp Asn Thr Leu Val Leu Gly Leu Leu Val Leu Ser Val Ala
 1 5 10 15

Ala Ser Ser Asn Asn Thr Ser Thr Ala Ser Thr Pro Ser Pro Ser Ser
 20 25 30

Ser Thr His Thr Ser Thr Thr Val Lys Ala Thr Thr Thr Ala Thr Thr
 35 40 45

Ser Thr Thr Thr Ala Thr Ser Thr Thr Ser Ser Thr Thr Ser Thr Lys
 50 55 60

Pro Gly Ser Thr Thr His Asp Pro Asn Val Met Arg Pro His Ala His
 65 70 75 80

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ccgatgcc cagtgcctgc cactgtgcc gccgcctgt ccatcctgtc caccatgcag 1680
cccagcacc tggaaacct ccccgacctg ttctgcctgc ccctgggcca gagcttcagc 1740
gccctgacag tgtccgagca cgtgtcctac gtggtcacca accagtaacct gatcaagggc 1800
atcagctacc ccgtgtccac caccgtcgtg ggccagagcc tgatcatcac ccagaccgac 1860
agccagacca agtgcgagct gacccggaac atgcacacca cacacagcat cactgccgcc 1920
ctgaacatca gcctggaaaa ctgcgccttc tgccagtctg ccctgctgga atacgacgat 1980
accagggcgg tgatcaacat catgtacatg cagcacagcg acgacgtgct gttgcctctg 2040
gacccctaca acgaggtggt ggtgtccagc ccccgaccc actacctgat gctgctgaag 2100
aacggcaccg tgctggaagt gaccgacgtg gtggtggacg ccaccgacag cagactgctg 2160
atgatgagcg tgtacgcct gagcgcctac atcgcatct acctgctgta ccggatgctg 2220
aaaacctgct ga 2232

```

```

<210> SEQ ID NO 8
<211> LENGTH: 743
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: gH consensus amino acid sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

```

```

<400> SEQUENCE: 8

```

```

Xaa Arg Pro Gly Leu Pro Ser Tyr Leu Thr Val Phe Ala Val Tyr Leu
1           5           10          15
Leu Ser His Leu Pro Ser Gln Arg Tyr Gly Ala Asp Ala Ala Ser Glu
20          25          30
Ala Leu Asp Pro His Ala Phe His Leu Leu Leu Asn Thr Tyr Gly Arg
35          40          45
Pro Ile Arg Phe Leu Arg Glu Asn Thr Thr Gln Cys Thr Tyr Asn Ser
50          55          60
Ser Leu Arg Asn Ser Thr Val Val Arg Glu Asn Ala Ile Ser Phe Asn
65          70          75          80
Phe Phe Gln Ser Tyr Asn Gln Tyr Tyr Val Phe His Met Pro Arg Cys
85          90          95
Leu Phe Ala Gly Pro Leu Ala Glu Gln Phe Leu Asn Gln Val Asp Leu
100         105         110
Thr Glu Thr Leu Glu Arg Tyr Gln Gln Arg Leu Asn Thr Tyr Ala Leu
115         120         125
Val Ser Lys Asp Leu Ala Ser Tyr Arg Ser Phe Ser Gln Gln Leu Lys
130         135         140
Ala Gln Asp Ser Leu Gly Glu Gln Pro Thr Thr Val Pro Pro Pro Ile
145         150         155         160
Asp Leu Ser Ile Pro His Val Trp Met Pro Pro Gln Thr Thr Pro His
165         170         175
Gly Trp Lys Glu Ser His Thr Thr Ser Gly Leu His Arg Pro His Phe
180         185         190
Asn Gln Thr Cys Ile Leu Phe Asp Gly His Asp Leu Leu Phe Ser Thr
195         200         205
Val Thr Pro Cys Leu His Gln Gly Phe Tyr Leu Ile Asp Glu Leu Arg
210         215         220

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Tyr Val Lys Ile Thr Leu Thr Glu Asp Phe Phe Val Val Thr Val Ser
 225 230 235 240
 Ile Asp Asp Asp Thr Pro Met Leu Leu Ile Phe Gly His Leu Pro Arg
 245 250 255
 Val Leu Phe Lys Ala Pro Tyr Gln Arg Asp Asn Phe Ile Leu Arg Gln
 260 265 270
 Thr Glu Lys His Glu Leu Leu Val Leu Val Lys Lys Asp Gln Leu Asn
 275 280 285
 Arg His Ser Tyr Leu Lys Asp Pro Asp Phe Leu Asp Ala Ala Leu Asp
 290 295 300
 Phe Asn Tyr Leu Asp Leu Ser Ala Leu Leu Arg Asn Ser Phe His Arg
 305 310 315 320
 Tyr Ala Val Asp Val Leu Lys Ser Gly Arg Cys Gln Met Leu Asp Arg
 325 330 335
 Arg Thr Val Glu Met Ala Phe Ala Tyr Ala Leu Ala Leu Phe Ala Ala
 340 345 350
 Ala Arg Gln Glu Glu Ala Gly Ala Glu Val Ser Val Pro Arg Ala Leu
 355 360 365
 Asp Arg Gln Ala Ala Leu Leu Gln Ile Gln Glu Phe Met Ile Thr Cys
 370 375 380
 Leu Ser Gln Thr Pro Pro Arg Thr Thr Leu Leu Leu Tyr Pro Thr Ala
 385 390 395 400
 Val Asp Leu Ala Lys Arg Ala Leu Trp Thr Pro Asn Gln Ile Thr Asp
 405 410 415
 Ile Thr Ser Leu Val Arg Leu Val Tyr Ile Leu Ser Lys Gln Asn Gln
 420 425 430
 Gln His Leu Ile Pro Gln Trp Ala Leu Arg Gln Ile Ala Asp Phe Ala
 435 440 445
 Leu Lys Leu His Lys Thr His Leu Ala Ser Phe Leu Ser Ala Phe Ala
 450 455 460
 Arg Gln Glu Leu Tyr Leu Met Gly Ser Leu Val His Ser Met Leu Val
 465 470 475 480
 His Thr Thr Glu Arg Arg Glu Ile Phe Ile Val Glu Thr Gly Leu Cys
 485 490 495
 Ser Leu Ala Glu Leu Ser His Phe Thr Gln Leu Leu Ala His Pro His
 500 505 510
 His Glu Tyr Leu Ser Asp Leu Tyr Thr Pro Cys Ser Ser Ser Gly Arg
 515 520 525
 Arg Asp His Ser Leu Glu Arg Leu Thr Arg Leu Phe Pro Asp Ala Thr
 530 535 540
 Val Pro Ala Thr Val Pro Ala Ala Leu Ser Ile Leu Ser Thr Met Gln
 545 550 555 560
 Pro Ser Thr Leu Glu Thr Phe Pro Asp Leu Phe Cys Leu Pro Leu Gly
 565 570 575
 Glu Ser Phe Ser Ala Leu Thr Val Ser Glu His Val Ser Tyr Val Val
 580 585 590
 Thr Asn Gln Tyr Leu Ile Lys Gly Ile Ser Tyr Pro Val Ser Thr Thr
 595 600 605
 Val Val Gly Gln Ser Leu Ile Ile Thr Gln Thr Asp Ser Gln Thr Lys
 610 615 620
 Cys Glu Leu Thr Arg Asn Met His Thr Thr His Ser Ile Thr Ala Ala
 625 630 635 640
 Leu Asn Ile Ser Leu Glu Asn Cys Ala Phe Cys Gln Ser Ala Leu Leu

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	645		650		655									
Glu Tyr Asp Asp Thr Gln Gly Val Ile Asn Ile Met Tyr Met His Asp														
	660					665				670				
Ser Asp Asp Val Leu Phe Ala Leu Asp Pro Tyr Asn Glu Val Val Val						680				685				
Ser Ser Pro Arg Thr His Tyr Leu Met Leu Leu Lys Asn Gly Thr Val						695				700				
Leu Glu Val Thr Asp Val Val Val Asp Ala Thr Asp Ser Arg Leu Leu						710				715				720
Met Met Ser Val Tyr Ala Leu Ser Ala Ile Ile Gly Ile Tyr Leu Leu						725				730				735
Tyr Arg Met Leu Lys Thr Cys						740								

<210> SEQ ID NO 9
 <211> LENGTH: 837
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: gL consensus nucleic acid sequence
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(3)
 <223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 9

```

nnntgcaggc ggccccactg cggcttcagc ttcagccctg gccccgtgat cctgctgtgg      60
tgctgcctgc tgctgcccac cgtgtcctct gccgcctgtg ctgtggcccc tacagccgcc      120
gagaaggtgc cagccgagtg ccttgagctg accagacggt gtctgctggg cgaggtgttc      180
cagggcgata agtacgagag ctggctgctg cccctgggtca acgtgaccgg cagagatggc      240
cccctgagcc agctgatccg gtacagaccg gtgaccctct aggccgcca cagcgtgctg      300
ctggacgaag cctttctgga cacactggcc ctgctgtaca acaacccga ccagctgctg      360
gccctgctga cactgctgag cagcgatacc gccccagat ggatgaccgt gatgctggggc      420
tacagcgagt gcggcgacgg atctcccgcc gtgtacacct gtgtggaaga cctgtgccgg      480
ggctacgacc tgaccagact gagctacggc cggtcctatc tcacagagca cgtgctggggc      540
ttcgagctgg tgccccccag cctgttcaat gtggtggtgg ccatccggaa cgaggccacc      600
cggaccaaca gagcagtgcg gctgcctgtg tccaccgctg ctgctccaga gggcatcacc      660
ctgttctacg gcctgtacaa cgccgtgaaa gagttctgcc tgagacacca gctggacccc      720
cccctgctgc ggcacctgga caagtactac gccggcctgc ctcccagact gaagcagacc      780
agagtgaacc tgccccccca cagcagatac ggcctcagg ccgtggacgc cagatga      837
    
```

<210> SEQ ID NO 10
 <211> LENGTH: 278
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: gL consensus amino acid sequence
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)..(1)
 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 10

```

Xaa Cys Arg Arg Pro Asp Cys Gly Phe Ser Phe Ser Pro Gly Pro Val
1           5           10           15
    
```

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Ile Leu Leu Trp Cys Cys Leu Leu Leu Pro Ile Val Ser Ser Ala Ala
20 25 30

Val Ser Val Ala Pro Thr Ala Ala Glu Lys Val Pro Ala Glu Cys Pro
35 40 45

Glu Leu Thr Arg Arg Cys Leu Leu Gly Glu Val Phe Gln Gly Asp Lys
50 55 60

Tyr Glu Ser Trp Leu Arg Pro Leu Val Asn Val Thr Gly Arg Asp Gly
65 70 75 80

Pro Leu Ser Gln Leu Ile Arg Tyr Arg Pro Val Thr Pro Glu Ala Ala
85 90 95

Asn Ser Val Leu Leu Asp Glu Ala Phe Leu Asp Thr Leu Ala Leu Leu
100 105 110

Tyr Asn Asn Pro Asp Gln Leu Arg Ala Leu Leu Thr Leu Leu Ser Ser
115 120 125

Asp Thr Ala Pro Arg Trp Met Thr Val Met Arg Gly Tyr Ser Glu Cys
130 135 140

Gly Asp Gly Ser Pro Ala Val Tyr Thr Cys Val Asp Asp Leu Cys Arg
145 150 155 160

Gly Tyr Asp Leu Thr Arg Leu Ser Tyr Gly Arg Ser Ile Phe Thr Glu
165 170 175

His Val Leu Gly Phe Glu Leu Val Pro Pro Ser Leu Phe Asn Val Val
180 185 190

Val Ala Ile Arg Asn Glu Ala Thr Arg Thr Asn Arg Ala Val Arg Leu
195 200 205

Pro Val Ser Thr Ala Ala Ala Pro Glu Gly Ile Thr Leu Phe Tyr Gly
210 215 220

Leu Tyr Asn Ala Val Lys Glu Phe Cys Leu Arg His Gln Leu Asp Pro
225 230 235 240

Pro Leu Leu Arg His Leu Asp Lys Tyr Tyr Ala Gly Leu Pro Pro Glu
245 250 255

Leu Lys Gln Thr Arg Val Asn Leu Pro Ala His Ser Arg Tyr Gly Pro
260 265 270

Gln Ala Val Asp Ala Arg
275

<210> SEQ ID NO 11
<211> LENGTH: 1419
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: gO consensus nucleic acid sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(3)
<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 11

```

nnnggcaaga aagaaatgat catggccaag ggcaccccca agatcatgct gctgatcagc      60
atcacctttc tgctgctgag cctgatcaac tgcaacgtgc tggtaaacag caagggcaca      120
cggcggagct ggcacctacac cgtgctgagc taccggggca aagagatcct gaagaagcag      180
aaagaggaca tcctgaagcg gctgatgagc accagcagcg acggctaccg gttcctgatg      240
taccacagcc agcagaaatt ccacgccatc gtgatcagca tggacaagtt cccccaggac      300
tacatcctgg ccggaccat ccggaacgac agcatcacc acatgtggtt cgacttctac      360
agcaccagc tgcggaagcc cgccaatac gtgtacagcg agtacaacca caccgccacc      420

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aagatcacc tgcggcctcc cccttgccgc accgtgccca gcatgaactg cctgagcgag 480
atgctgaacg tgtccaagcg gaacgacacc ggcgagaagg gctgcgcaa cttcaccacc 540
ttcaacccca tgttcttcaa cgtgccccgg tggaacacca agctgtacat cggcagcaac 600
aaagtgaacg tggacagcca gaccatctac tttctgggcc tgaccgccct gctgctgcgc 660
tacgcccaga gaaactgcac ccggctcttc tacctgggtca acgcatgag ccggaacctg 720
ttccgggtgc ccaagtacat caacggcacc aagctgaaga acaccatgcg gaagctgaag 780
cggaagcagg ccctgggtcaa agagcagccc cagaagaaga acaagaagtc ccagagcacc 840
accacccctc acctgagcta caccaccagc accgccttca acgtgaccac caactgacc 900
tacagcgcca cagccgctg gaccagagtg gccacctcca ccaccggcta ccggcccagc 960
agcaacttca tgaagtccat catggccacc cagctgaggg acctggccac ctgggtgtac 1020
accaccctgc ggtacagaaa cgagcccttc tgcaagcccg accggaacag aaccgccgtg 1080
tccgagttca tgaagaatac ccacgtgctg atccgcaacg agacacccta caccatctac 1140
ggcaccctgg acatgagcag cctgtactac aacgagacaa tgagcgtcga gaacgagaca 1200
gccagcgaca acaacgaac caccaccacc agccccagca cccgggtcca gcggaccttc 1260
atcgaccccc tgtgggacta cctggacagc ctgctgttcc tggacaagat ccggaacttc 1320
agcctgcagc tgcccgccta cggcaacctg acccccctg aacacagaag ggccgccaac 1380
ctgagcacc tgaacagcct gtggtggtgg ctgcagtga 1419

```

<210> SEQ ID NO 12

<211> LENGTH: 472

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: g0 consensus amino acid sequence

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(1)

<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 12

```

Xaa Gly Lys Lys Glu Met Ile Met Val Lys Gly Ile Pro Lys Ile Met
1          5          10          15
Leu Leu Ile Ser Ile Thr Phe Leu Leu Leu Ser Leu Ile Asn Cys Asn
20          25          30
Val Leu Val Asn Ser Lys Gly Thr Arg Arg Ser Trp Pro Tyr Thr Val
35          40          45
Leu Ser Tyr Arg Gly Lys Glu Ile Leu Lys Lys Gln Lys Glu Asp Ile
50          55          60
Leu Lys Arg Leu Met Ser Thr Ser Ser Asp Gly Tyr Arg Phe Leu Met
65          70          75          80
Tyr Pro Ser Gln Gln Lys Phe His Ala Ile Val Ile Ser Met Asp Lys
85          90          95
Phe Pro Gln Asp Tyr Ile Leu Ala Gly Pro Ile Arg Asn Asp Ser Ile
100         105         110
Thr His Met Trp Phe Asp Phe Tyr Ser Thr Gln Leu Arg Lys Pro Ala
115         120         125
Lys Tyr Val Tyr Ser Glu Tyr Asn His Thr Ala His Lys Ile Thr Leu
130         135         140
Arg Pro Pro Pro Cys Gly Thr Val Pro Ser Met Asn Cys Leu Ser Glu
145         150         155         160
Met Leu Asn Val Ser Lys Arg Asn Asp Thr Gly Glu Lys Gly Cys Gly

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165				170				175							
Asn	Phe	Thr	Thr	Phe	Asn	Pro	Met	Phe	Phe	Asn	Val	Pro	Arg	Trp	Asn
			180								185				190
Thr	Lys	Leu	Tyr	Ile	Gly	Ser	Asn	Lys	Val	Asn	Val	Asp	Ser	Gln	Thr
			195								200				205
Ile	Tyr	Phe	Leu	Gly	Leu	Thr	Ala	Leu	Leu	Leu	Arg	Tyr	Ala	Gln	Arg
			210				215				220				
Asn	Cys	Thr	Arg	Ser	Phe	Tyr	Leu	Val	Asn	Ala	Met	Ser	Arg	Asn	Leu
			225				230				235				240
Phe	Arg	Val	Pro	Lys	Tyr	Ile	Asn	Gly	Thr	Lys	Leu	Lys	Asn	Thr	Met
			245								250				255
Arg	Lys	Leu	Lys	Arg	Lys	Gln	Ala	Leu	Val	Lys	Glu	Gln	Pro	Gln	Lys
			260								265				270
Lys	Asn	Lys	Lys	Ser	Gln	Ser	Thr	Thr	Thr	Pro	Tyr	Leu	Ser	Tyr	Thr
			275				280								285
Thr	Ser	Thr	Ala	Phe	Asn	Val	Thr	Thr	Asn	Val	Thr	Tyr	Ser	Ala	Thr
			290				295				300				
Ala	Ala	Val	Thr	Arg	Val	Ala	Thr	Ser	Thr	Thr	Gly	Tyr	Arg	Pro	Asp
			305				310				315				320
Ser	Asn	Phe	Met	Lys	Ser	Ile	Met	Ala	Thr	Gln	Leu	Arg	Asp	Leu	Ala
			325								330				335
Thr	Trp	Val	Tyr	Thr	Thr	Leu	Arg	Tyr	Arg	Asn	Glu	Pro	Phe	Cys	Lys
			340								345				350
Pro	Asp	Arg	Asn	Arg	Thr	Ala	Val	Ser	Glu	Phe	Met	Lys	Asn	Thr	His
			355				360								365
Val	Leu	Ile	Arg	Asn	Glu	Thr	Pro	Tyr	Thr	Ile	Tyr	Gly	Thr	Leu	Asp
			370				375				380				
Met	Ser	Ser	Leu	Tyr	Tyr	Asn	Glu	Thr	Met	Ser	Val	Glu	Asn	Glu	Thr
			385				390				395				400
Ala	Ser	Asp	Asn	Asn	Glu	Thr	Thr	Pro	Thr	Ser	Pro	Ser	Thr	Arg	Phe
			405								410				415
Gln	Arg	Thr	Phe	Ile	Asp	Pro	Leu	Trp	Asp	Tyr	Leu	Asp	Ser	Leu	Leu
			420								425				430
Phe	Leu	Asp	Lys	Ile	Arg	Asn	Phe	Ser	Leu	Gln	Leu	Pro	Ala	Tyr	Gly
			435				440								445
Asn	Leu	Thr	Pro	Pro	Glu	His	Arg	Arg	Ala	Ala	Asn	Leu	Ser	Thr	Leu
			450				455				460				
Asn	Ser	Leu	Trp	Trp	Leu	Gln									
			465				470								

<210> SEQ ID NO 13

<211> LENGTH: 516

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: UL128 consensus nucleic acid sequence

<220> FEATURE:

<221> NAME/KEY: misc_feature

<222> LOCATION: (1)..(3)

<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 13

nnnagcccca aggatctgac ccctttctctg accgcctgt ggctgctctt gggccacagc 60

agagtgccta gagtgcgggc cgaggaatgc tgcgagtcca tcaacgtgaa ccaccccccc 120

gagcgggtgct acgacttcaa gatgtgcaac cggttcaacc tggtcttgag atgccccgac 180

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ggcgaagtgt gctacagccc cgagaaaacc gccgagatcc ggggcatcgt gaccaccatg 240
accacagccc tgaccagaca ggtggtgcat aacaagctga ccagttgcaa ctacaacccc 300
ctgtacctgg aagccgacgg ccggatcaga tgcggcaaag tgaacgacaa ggcccagtac 360
ctgctggggc ctgcaggcag tgtgccctac agatggatca acctggaata cgacaagatc 420
accgggatcg tgggcctgga ccagtacctg gaaagcgtga agaagcacia gcggtctggac 480
gtgtgccggg ccaagatggg ctacatgctg cagtga 516

```

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<210> SEQ ID NO 14
<211> LENGTH: 171
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: UL128 consensus amino acid sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

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<400> SEQUENCE: 14

```

```

Xaa Ser Pro Lys Asp Leu Thr Pro Phe Leu Thr Ala Leu Trp Leu Leu
1          5          10          15
Leu Gly His Ser Arg Val Pro Arg Val Arg Ala Glu Glu Cys Cys Glu
20        25        30
Phe Ile Asn Val Asn His Pro Pro Glu Arg Cys Tyr Asp Phe Lys Met
35        40        45
Cys Asn Arg Phe Thr Val Ala Leu Arg Cys Pro Asp Gly Glu Val Cys
50        55        60
Tyr Ser Pro Glu Lys Thr Ala Glu Ile Arg Gly Ile Val Thr Thr Met
65        70        75        80
Thr His Ser Leu Thr Arg Gln Val Val His Asn Lys Leu Thr Ser Cys
85        90        95
Asn Tyr Asn Pro Leu Tyr Leu Glu Ala Asp Gly Arg Ile Arg Cys Gly
100       105       110
Lys Val Asn Asp Lys Ala Gln Tyr Leu Leu Gly Ala Ala Gly Ser Val
115       120       125
Pro Tyr Arg Trp Ile Asn Leu Glu Tyr Asp Lys Ile Thr Arg Ile Val
130       135       140
Gly Leu Asp Gln Tyr Leu Glu Ser Val Lys Lys His Lys Arg Leu Asp
145       150       155       160
Val Cys Arg Ala Lys Met Gly Tyr Met Leu Gln
165       170

```

```

<210> SEQ ID NO 15
<211> LENGTH: 646
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: UL130 consensus amino acid sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(3)
<223> OTHER INFORMATION: n is a, c, g, or t

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<400> SEQUENCE: 15

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```

nngtctgcgg ctgctgctgc ggcaccactt ccaactgcctg ctgctgtgtg ccgtgtgggc 60
cacccttgt ctggccagcc cttggagcac cctgaccgcc aaccagaacc ctagccccc 120
ctggtccaag ctgacctaca gcaagcccca cgacgccgct accttctact gccattct 180

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gtaccccagc cctcccagaa gccccctgca gttcagcggc ttccagcggg tgtccaccgg 240
cctgagtgcc cggaacgaga cactgtacct gctgtacaac cgcgagggcc agaccctggt 300
ggaacggctc agcacctggg tcaagaaagt gatctggtat ctgagcggcc ggaaccagac 360
catcctgcag cggatgcctc ggaccgccag caagcctagc gacggcaacg tgcagatcag 420
cgtggaagat gccaaaatct tcggcgccca catggtgccc aagcagacca agctgctgag 480
attcgtggtc aacgacggca ccagatacca gatgtgcgtg atgaagctgg aaagctgggc 540
ccacgtgttc cgggactaca gcgtgtcatt ccaggtccga ctgaccttca ccgaggccaa 600
caaccagacc tacaccttct gacccaccc caacctgac gtctga 646

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<210> SEQ ID NO 16
<211> LENGTH: 214
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: UL130 consensus amino acid sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

```

```

<400> SEQUENCE: 16

```

```

Xaa Leu Arg Leu Leu Leu Arg His His Phe His Cys Leu Leu Leu Cys
1          5          10          15
Ala Val Trp Ala Thr Pro Cys Leu Ala Ser Pro Trp Ser Thr Leu Thr
20          25          30
Ala Asn Gln Asn Pro Ser Pro Pro Trp Ser Lys Leu Thr Tyr Ser Lys
35          40          45
Pro His Asp Ala Ala Thr Phe Tyr Cys Pro Phe Leu Tyr Pro Ser Pro
50          55          60
Pro Arg Ser Pro Leu Gln Phe Ser Gly Phe Gln Arg Val Ser Thr Gly
65          70          75          80
Pro Glu Cys Arg Asn Glu Thr Leu Tyr Leu Leu Tyr Asn Arg Glu Gly
85          90          95
Gln Thr Leu Val Glu Arg Ser Ser Thr Trp Val Lys Lys Val Ile Trp
100         105         110
Tyr Leu Ser Gly Arg Asn Gln Thr Ile Leu Gln Arg Met Pro Arg Thr
115         120         125
Ala Ser Lys Pro Ser Asp Gly Asn Val Gln Ile Ser Val Glu Asp Ala
130         135         140
Lys Ile Phe Gly Ala His Met Val Pro Lys Gln Thr Lys Leu Leu Arg
145         150         155         160
Phe Val Val Asn Asp Gly Thr Arg Tyr Gln Met Cys Val Met Lys Leu
165         170         175
Glu Ser Trp Ala His Val Phe Arg Asp Tyr Ser Val Ser Phe Gln Val
180         185         190
Arg Leu Thr Phe Thr Glu Ala Asn Asn Gln Thr Tyr Thr Phe Cys Thr
195         200         205
His Pro Asn Leu Ile Val
210

```

```

<210> SEQ ID NO 17
<211> LENGTH: 390
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: UL131a consensus nucleic acid sequence

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<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(3)
<223> OTHER INFORMATION: n is a, c, g, or t

<400> SEQUENCE: 17

nnnagactgt gcagagtgtg gctgagcgtg tgcctgtgcg ccgtggtgct gggccagtgc      60
cagagagaga cagccgagaa gaacgactac taccgggtgc cccactactg ggacgcctgc      120
tctagagccc tgccccacca gaccgggtac aaatacgtgg aacagctggt ggacctgacc      180
ctgaactacc actacgacgc cagccacggc ctggacaact tcgacgtgct gaagcgggat      240
aacgtgacgc aggtgtccct gctgatcagc gacttccggc ggcagaacag aagaggcggc      300
accaacaagc ggactacctt caacgcccgt ggcagcctgg cccctcacgc cagatccctg      360
gaattcagcg tgcggctggt cgccaactga      390

```

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<210> SEQ ID NO 18
<211> LENGTH: 129
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: UL131a consensus amino acid sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

```

```

<400> SEQUENCE: 18

Xaa Arg Leu Cys Arg Val Trp Leu Ser Val Cys Leu Cys Ala Val Val
1          5          10          15

Leu Gly Gln Cys Gln Arg Glu Thr Ala Glu Lys Asn Asp Tyr Tyr Arg
20          25          30

Val Pro His Tyr Trp Asp Ala Cys Ser Arg Ala Leu Pro Asp Gln Thr
35          40          45

Arg Tyr Lys Tyr Val Glu Gln Leu Val Asp Leu Thr Leu Asn Tyr His
50          55          60

Tyr Asp Ala Ser His Gly Leu Asp Asn Phe Asp Val Leu Lys Arg Ile
65          70          75          80

Asn Val Thr Glu Val Ser Leu Leu Ile Ser Asp Phe Arg Arg Gln Asn
85          90          95

Arg Arg Gly Gly Thr Asn Lys Arg Thr Thr Phe Asn Ala Ala Gly Ser
100         105         110

Leu Ala Pro His Ala Arg Ser Leu Glu Phe Ser Val Arg Leu Phe Ala
115         120         125

Asn

```

```

<210> SEQ ID NO 19
<211> LENGTH: 1687
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: UL83 consensus nucleic acid sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(3)
<223> OTHER INFORMATION: n is a, c, g, or t

```

```

<400> SEQUENCE: 19

nnntgagagt cgcggggcga gatgcctga aatgatcagc gtgctgggcc caatttcgg      60
gcatgtgctg aaggccgtct tctcccggg agacaccccc gtgctgectc acgagacaag      120

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actgctgcag actggcatcc atgtgaggggt ctcccagcca tctctgattc tgggtgtctca 180
gtacacccca gatagtacac cctgccacag aggggacaac cagctgcagg tgcagcatac 240
ctacttcacc ggatcagagg tcgaaaatgt gagcgtcaac gtgcacaatc ccacaggcag 300
gagtatctgt ccttcacagg agccaatgag catctactgt tacgcctctgc ccctgaaaat 360
gctgaacatc cctagcatta atgtgcacca ttaccctctcc gccgctgaac gaaagcaccg 420
gcatctgcct gtggcagatg ccgtcatcca tgcttcaggc aaacagatgt ggcaggcacg 480
actgaccgtg agcggactgg catggacacg acagcagaac cagtggaagg agccagacgt 540
gtactatact agcgcctctg tgttccccac caaagacgtg gccctgcgac acgtggtctg 600
cgcacatgag ctggtgtgct ctatggaaaa tactcgggcc accaagatgc aggtcattgg 660
cgatcagtac gtcaaagtgt atctggagtc cttttgtgaa gacgtgccct ctgggaagct 720
gttcatgcac gtgaccctgg gaagcgatgt cgaggaagac ctgactatga cccggaaccc 780
acagcccttt atgagacctc acgagaggaa cggttctact gtgctgtgcc caaagaatat 840
gatcattaag cccgggaaaa tctctcatat tatgctggat gtggccttta caagtcacga 900
gcatttcgga ctgctgtgcc ccaaaagcat ccctgggctg tcaattagcg gaaacctgct 960
gatgaatggc cagcagatct ttctggaagt gcaggccatt cgagagaccg tcgaactgcg 1020
acagtacgac ccagtggcag ccctgttctt ttctgatatc gacctgtctc tgcagagagg 1080
ccctcagtat agtgagcacc caacattcac ttcacagtac aggattcagg ggaagctgga 1140
gtatcggcac acttgggata gacatgacga aggagctgca cagggcgacg atgacgtgtg 1200
gacctccggc tctgatagtg acgaggaact ggtgaccaca gagcgaaaaa ctccccgggt 1260
gaccggagga ggagctatgg caggagcacc aaccagcgcg ggacgaaaga gaaaaagcgc 1320
cagcagcgcc acagcatgca ctgcaggcgt gatgacaagg gggcgcctga aggcagaatc 1380
cacagtcgcc cctgaggaag atactgacga ggattctgac aacgaaatcc acaatccagc 1440
cgtgttcacc tggccacctt ggcaggcagg aattctggct cgcaatctgg tccctatggt 1500
ggccactgtc cagggacaga acctgaagta ccaggagttt ttctgggatg ctaatgacat 1560
ctatcggatt ttcgagagc tggaaaggct gtggcagcca gcagctcagc caaaaaggcg 1620
ccgacacaga caggacgcac tgcttgacc atgtatcgcc tccaccccaa agaaacatag 1680
gggctga 1687

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```

<210> SEQ ID NO 20
<211> LENGTH: 561
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: UL83 consensus amino acid sequence
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)..(1)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

```

```

<400> SEQUENCE: 20

```

```

Xaa Glu Ser Arg Gly Arg Arg Cys Pro Glu Met Ile Ser Val Leu Gly
1           5           10          15
Pro Ile Ser Gly His Val Leu Lys Ala Val Phe Ser Arg Gly Asp Thr
                20          25          30
Pro Val Leu Pro His Glu Thr Arg Leu Leu Gln Thr Gly Ile His Val
                35          40          45
Arg Val Ser Gln Pro Ser Leu Ile Leu Val Ser Gln Tyr Thr Pro Asp
50          55          60

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Ser Thr Pro Cys His Arg Gly Asp Asn Gln Leu Gln Val Gln His Thr
 65 70 75 80
 Tyr Phe Thr Gly Ser Glu Val Glu Asn Val Ser Val Asn Val His Asn
 85 90 95
 Pro Thr Gly Arg Ser Ile Cys Pro Ser Gln Glu Pro Met Ser Ile Tyr
 100 105 110
 Val Tyr Ala Leu Pro Leu Lys Met Leu Asn Ile Pro Ser Ile Asn Val
 115 120 125
 His His Tyr Pro Ser Ala Ala Glu Arg Lys His Arg His Leu Pro Val
 130 135 140
 Ala Asp Ala Val Ile His Ala Ser Gly Lys Gln Met Trp Gln Ala Arg
 145 150 155 160
 Leu Thr Val Ser Gly Leu Ala Trp Thr Arg Gln Gln Asn Gln Trp Lys
 165 170 175
 Glu Pro Asp Val Tyr Tyr Thr Ser Ala Phe Val Phe Pro Thr Lys Asp
 180 185 190
 Val Ala Leu Arg His Val Val Cys Ala His Glu Leu Val Cys Ser Met
 195 200 205
 Glu Asn Thr Arg Ala Thr Lys Met Gln Val Ile Gly Asp Gln Tyr Val
 210 215 220
 Lys Val Tyr Leu Glu Ser Phe Cys Glu Asp Val Pro Ser Gly Lys Leu
 225 230 235 240
 Phe Met His Val Thr Leu Gly Ser Asp Val Glu Glu Asp Leu Thr Met
 245 250 255
 Thr Arg Asn Pro Gln Pro Phe Met Arg Pro His Glu Arg Asn Gly Phe
 260 265 270
 Thr Val Leu Cys Pro Lys Asn Met Ile Ile Lys Pro Gly Lys Ile Ser
 275 280 285
 His Ile Met Leu Asp Val Ala Phe Thr Ser His Glu His Phe Gly Leu
 290 295 300
 Leu Cys Pro Lys Ser Ile Pro Gly Leu Ser Ile Ser Gly Asn Leu Leu
 305 310 315 320
 Met Asn Gly Gln Gln Ile Phe Leu Glu Val Gln Ala Ile Arg Glu Thr
 325 330 335
 Val Glu Leu Arg Gln Tyr Asp Pro Val Ala Ala Leu Phe Phe Phe Asp
 340 345 350
 Ile Asp Leu Leu Leu Gln Arg Gly Pro Gln Tyr Ser Glu His Pro Thr
 355 360 365
 Phe Thr Ser Gln Tyr Arg Ile Gln Gly Lys Leu Glu Tyr Arg His Thr
 370 375 380
 Trp Asp Arg His Asp Glu Gly Ala Ala Gln Gly Asp Asp Asp Val Trp
 385 390 395 400
 Thr Ser Gly Ser Asp Ser Asp Glu Glu Leu Val Thr Thr Glu Arg Lys
 405 410 415
 Thr Pro Arg Val Thr Gly Gly Gly Ala Met Ala Gly Ala Ser Thr Ser
 420 425 430
 Ala Gly Arg Lys Arg Lys Ser Ala Ser Ser Ala Thr Ala Cys Thr Ala
 435 440 445
 Gly Val Met Thr Arg Gly Arg Leu Lys Ala Glu Ser Thr Val Ala Pro
 450 455 460
 Glu Glu Asp Thr Asp Glu Asp Ser Asp Asn Glu Ile His Asn Pro Ala
 465 470 475 480

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gaggcttggt gtgtggacca gcggcggacc ctggaagtgt tcaaagagct gagcaagatc 1620
aaccaccagcg ccatoctgag cgccatctac aacaagccta tcgcccgcag attcatgggc 1680
gacgtgctgg gcctggccag ctgcgtgacc atcaaccaga ccagcgtgaa ggtgctgcgg 1740
gacatgaaog tgaagaaag ccccggcaga tgctactcca gaccogtggg catcttcaac 1800
ttcgccaaca gctcctacgt gcagtaggc cagctgggag aggacaacga gatcctgctg 1860
ggaaaccacc ggaccgagga atgccagctg cccagcctga agatctttat cgccggcaac 1920
agcgcctaog agtatgtgga ctacctgttc aagcggatga tcgacctgag cagcatcagc 1980
accgtggaca gcatgatcgc cctggacatc gacccccctgg aaaacaccga cttccgggtg 2040
ctggaactgt acagccagaa agagctgagg agcagcaacg tgttcgacct ggaagagatc 2100
atgcgcgagt tcaacagcta caagcagcgc gtgaaatacg tcgaggacaa ggtggtggac 2160
cccctgcccc cctacctgaa gggcctggac gacctgatga gcggcctggg agctgctggc 2220
aaggccgtgg gagtggccat tggagctgtg ggcggagcgg tggccagcgt ggtggaaggc 2280
gtggccacct ttctgaagaa ccccttcggc gccttcacca tcatcctggg ggctatcgcc 2340
gtcgtgatca tcacctacct gatctacacc cggcagcggc ggctgtgtac ccagcctctg 2400
cagaacctgt tcccctacct ggtgtccgcc gacggcacca ccgtgacaag cggctccacc 2460
aaggacacca gcctgcaggc cccaccacgc tacgaggaat ccgtgtacaa cagcggccgg 2520
aagggccccag gccctcctag ctctgacgcc tctacagcgg ccccacccca caccaacgag 2580
caggcctacc agatgctgct ggccttggtt agactggacg ccgagcagag agcccagcag 2640
aacggaaccg acagcctgga tggccagacc ggcacccagg acaagggcca gaagcccaac 2700
ctgctggacc ggctgcggca cagaaagaac ggctaccggc acctgaagga cagcgcgaa 2760
gaggaaaaog tgtga 2775

```

<210> SEQ ID NO 22

<211> LENGTH: 924

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: IgE leader + gB consensus amino acid sequence

<400> SEQUENCE: 22

```

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Thr Arg Val
1           5           10           15
His Ser Glu Ser Arg Ile Trp Cys Leu Val Val Cys Val Asn Leu Cys
                20           25           30
Ile Val Cys Leu Gly Ala Ala Val Ser Ser Ser Ser Thr Arg Gly Thr
                35           40           45
Ser Ala Thr His Ser His His Ser Ser His Thr Thr Ser Ala Ala His
                50           55           60
Ser Arg Ser Gly Ser Val Ser Ser Gln Arg Val Thr Ser Ser Glu Ala
        65           70           75           80
Val Ser His Arg Ala Asn Glu Thr Ile Tyr Asn Thr Thr Leu Lys Tyr
                85           90           95
Gly Asp Val Val Gly Val Asn Thr Thr Lys Tyr Pro Tyr Arg Val Cys
                100           105           110
Ser Met Ala Gln Gly Thr Asp Leu Ile Arg Phe Glu Arg Asn Ile Val
                115           120           125
Cys Thr Ser Met Lys Pro Ile Asn Glu Asp Leu Asp Glu Gly Ile Met
        130           135           140

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Val	Val	Tyr	Lys	Arg	Asn	Ile	Val	Ala	His	Thr	Phe	Lys	Val	Arg	Val
145					150					155					160
Tyr	Gln	Lys	Val	Leu	Thr	Phe	Arg	Arg	Ser	Tyr	Ala	Tyr	Ile	His	Thr
				165					170					175	
Thr	Tyr	Leu	Leu	Gly	Ser	Asn	Thr	Glu	Tyr	Val	Ala	Pro	Pro	Met	Trp
			180					185					190		
Glu	Ile	His	His	Ile	Asn	Ser	His	Ser	Gln	Cys	Tyr	Ser	Ser	Tyr	Ser
		195					200					205			
Arg	Val	Ile	Ala	Gly	Thr	Val	Phe	Val	Ala	Tyr	His	Arg	Asp	Ser	Tyr
	210					215					220				
Glu	Asn	Lys	Thr	Met	Gln	Leu	Met	Pro	Asp	Asp	Tyr	Ser	Asn	Thr	His
225					230					235					240
Ser	Thr	Arg	Tyr	Val	Thr	Val	Lys	Asp	Gln	Trp	His	Ser	Arg	Gly	Ser
				245					250					255	
Thr	Trp	Leu	Tyr	Arg	Glu	Thr	Cys	Asn	Leu	Asn	Cys	Met	Val	Thr	Ile
			260					265					270		
Thr	Thr	Ala	Arg	Ser	Lys	Tyr	Pro	Tyr	His	Phe	Phe	Ala	Thr	Ser	Thr
		275					280					285			
Gly	Asp	Val	Val	Asp	Ile	Ser	Pro	Phe	Tyr	Asn	Gly	Thr	Asn	Arg	Asn
	290					295					300				
Ala	Ser	Tyr	Phe	Gly	Glu	Asn	Ala	Asp	Lys	Phe	Phe	Ile	Phe	Pro	Asn
305					310					315					320
Tyr	Thr	Ile	Val	Ser	Asp	Phe	Gly	Arg	Pro	Asn	Ser	Ala	Leu	Glu	Thr
				325					330					335	
His	Arg	Leu	Val	Ala	Phe	Leu	Glu	Arg	Ala	Asp	Ser	Val	Ile	Ser	Trp
			340					345					350		
Asp	Ile	Gln	Asp	Glu	Lys	Asn	Val	Thr	Cys	Gln	Leu	Thr	Phe	Trp	Glu
		355					360					365			
Ala	Ser	Glu	Arg	Thr	Ile	Arg	Ser	Glu	Ala	Glu	Asp	Ser	Tyr	His	Phe
	370					375					380				
Ser	Ser	Ala	Lys	Met	Thr	Ala	Thr	Phe	Leu	Ser	Lys	Lys	Gln	Glu	Val
385					390					395					400
Asn	Met	Ser	Asp	Ser	Ala	Leu	Asp	Cys	Val	Arg	Asp	Glu	Ala	Ile	Asn
				405					410					415	
Lys	Leu	Gln	Gln	Ile	Phe	Asn	Thr	Ser	Tyr	Asn	Gln	Thr	Tyr	Glu	Lys
			420					425					430		
Tyr	Gly	Asn	Val	Ser	Val	Phe	Glu	Thr	Thr	Gly	Gly	Leu	Val	Val	Phe
		435					440					445			
Trp	Gln	Gly	Ile	Lys	Gln	Lys	Ser	Leu	Val	Glu	Leu	Glu	Arg	Leu	Ala
	450					455					460				
Asn	Arg	Ser	Ser	Leu	Asn	Leu	Thr	His	Arg	Thr	Lys	Arg	Ser	Thr	Asp
465					470					475					480
Gly	Asn	Asn	Thr	Thr	His	Leu	Ser	Asn	Met	Glu	Ser	Val	His	Asn	Leu
				485					490					495	
Val	Tyr	Ala	Gln	Leu	Gln	Phe	Thr	Tyr	Asp	Thr	Leu	Arg	Gly	Tyr	Ile
			500					505					510		
Asn	Arg	Ala	Leu	Ala	Gln	Ile	Ala	Glu	Ala	Trp	Cys	Val	Asp	Gln	Arg
			515				520					525			
Arg	Thr	Leu	Glu	Val	Phe	Lys	Glu	Leu	Ser	Lys	Ile	Asn	Pro	Ser	Ala
	530					535					540				
Ile	Leu	Ser	Ala	Ile	Tyr	Asn	Lys	Pro	Ile	Ala	Ala	Arg	Phe	Met	Gly
545					550					555					560
Asp	Val	Leu	Gly	Leu	Ala	Ser	Cys	Val	Thr	Ile	Asn	Gln	Thr	Ser	Val

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565					570					575					
Lys	Val	Leu	Arg	Asp	Met	Asn	Val	Lys	Glu	Ser	Pro	Gly	Arg	Cys	Tyr
			580					585						590	
Ser	Arg	Pro	Val	Val	Ile	Phe	Asn	Phe	Ala	Asn	Ser	Ser	Tyr	Val	Gln
		595					600					605			
Tyr	Gly	Gln	Leu	Gly	Glu	Asp	Asn	Glu	Ile	Leu	Leu	Gly	Asn	His	Arg
	610					615					620				
Thr	Glu	Glu	Cys	Gln	Leu	Pro	Ser	Leu	Lys	Ile	Phe	Ile	Ala	Gly	Asn
625					630					635					640
Ser	Ala	Tyr	Glu	Tyr	Val	Asp	Tyr	Leu	Phe	Lys	Arg	Met	Ile	Asp	Leu
			645						650					655	
Ser	Ser	Ile	Ser	Thr	Val	Asp	Ser	Met	Ile	Ala	Leu	Asp	Ile	Asp	Pro
			660					665					670		
Leu	Glu	Asn	Thr	Asp	Phe	Arg	Val	Leu	Glu	Leu	Tyr	Ser	Gln	Lys	Glu
		675					680						685		
Leu	Arg	Ser	Ser	Asn	Val	Phe	Asp	Leu	Glu	Glu	Ile	Met	Arg	Glu	Phe
690					695						700				
Asn	Ser	Tyr	Lys	Gln	Arg	Val	Lys	Tyr	Val	Glu	Asp	Lys	Val	Val	Asp
705				710						715					720
Pro	Leu	Pro	Pro	Tyr	Leu	Lys	Gly	Leu	Asp	Asp	Leu	Met	Ser	Gly	Leu
				725					730						735
Gly	Ala	Ala	Gly	Lys	Ala	Val	Gly	Val	Ala	Ile	Gly	Ala	Val	Gly	Gly
			740					745						750	
Ala	Val	Ala	Ser	Val	Val	Glu	Gly	Val	Ala	Thr	Phe	Leu	Lys	Asn	Pro
		755					760						765		
Phe	Gly	Ala	Phe	Thr	Ile	Ile	Leu	Val	Ala	Ile	Ala	Val	Val	Ile	Ile
770						775					780				
Thr	Tyr	Leu	Ile	Tyr	Thr	Arg	Gln	Arg	Arg	Leu	Cys	Thr	Gln	Pro	Leu
785					790					795					800
Gln	Asn	Leu	Phe	Pro	Tyr	Leu	Val	Ser	Ala	Asp	Gly	Thr	Thr	Val	Thr
				805					810						815
Ser	Gly	Ser	Thr	Lys	Asp	Thr	Ser	Leu	Gln	Ala	Pro	Pro	Ser	Tyr	Glu
			820					825					830		
Glu	Ser	Val	Tyr	Asn	Ser	Gly	Arg	Lys	Gly	Pro	Gly	Pro	Pro	Ser	Ser
		835					840						845		
Asp	Ala	Ser	Thr	Ala	Ala	Pro	Pro	Tyr	Thr	Asn	Glu	Gln	Ala	Tyr	Gln
850						855					860				
Met	Leu	Leu	Ala	Leu	Ala	Arg	Leu	Asp	Ala	Glu	Gln	Arg	Ala	Gln	Gln
865					870					875					880
Asn	Gly	Thr	Asp	Ser	Leu	Asp	Gly	Gln	Thr	Gly	Thr	Gln	Asp	Lys	Gly
				885					890						895
Gln	Lys	Pro	Asn	Leu	Leu	Asp	Arg	Leu	Arg	His	Arg	Lys	Asn	Gly	Tyr
			900					905						910	
Arg	His	Leu	Lys	Asp	Ser	Asp	Glu	Glu	Glu	Asn	Val				
		915						920							

<210> SEQ ID NO 23

<211> LENGTH: 1170

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: IgE leader + gM consensus nucleic acid sequence

<400> SEQUENCE: 23

atggattgga cctggatcct gttcctggtg gccgctgcta cccgggtcca cagtgcaccc 60

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agccacgtgg acaaagtga caccceggact tggagcgcca gcacgtgtt catggtgctg 120
accttcgtga atgtgtccgt ccacctggg ctgagcaact tccccacct gggetacccc 180
tgcgtgtact accacgtggt ggacttcgag cggctgaaca tgagcgcta caacgtgatg 240
catctgcaca ccccatgct gttctggac agcgtgcagc tcgtgtgcta cgccgtgtt 300
atgcagctgg tgttcctggc cgtgaccatc tactacctcg tgtgtggat caagatttct 360
atgcggaagg acaagggcat gacccctgaac cagagcacc gggacatcag ctacatgggc 420
gacagcctga ccgcttctc gttcctctg agcatggaca ccttcagct gttcacctg 480
accatgagct tccggctgcc cagcatgatc gccttatgg ccgccgtcca cttctctgt 540
ctgaccatct tcaacgtgtc catggtcacc cagtacagaa gctacaagcg gagcctgtc 600
ttcttcagtc ggctgcaccc caagctgaag ggcaccgtcc agttccggac cctgatcgtg 660
aacctggtgg aagtggccct gggcttcaac accacgtgg tggctatggc tctgtgctac 720
ggcttcggca acaacttctt cgtgcggaca ggcacatgg tgctggccgt gttcgtggg 780
tacgccatta tcagcatcat ctactttctg ctgatcgagg ccgtgttctt ccagtacgtg 840
aaggtgcagt tcggctacca cctggggccc ttttccggc tgtgcccct gatctacccc 900
atcgtgcagt acgacacctt cctgagcaac gagtaccgga ccggcatcag ctggtcctc 960
ggcatgctgt tcttcctctg ggccatgttc accacctgtc gggccgtgcg gtacttcaga 1020
ggcagaggca gcggctccgt gaagtaccag gccctggcca cagccagcgg cgaagaagtg 1080
gccgccctga gccaccacga cagcctggaa agcagacggc tgagagagga agaggacgac 1140
gacgacgatg aggacttoga ggacgctga 1170

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<210> SEQ ID NO 24

<211> LENGTH: 389

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: IgE leader + gM consensus amino acid sequence

<400> SEQUENCE: 24

```

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
 1             5             10             15
His Ser Ala Pro Ser His Val Asp Lys Val Asn Thr Arg Thr Trp Ser
                20             25             30
Ala Ser Ile Val Phe Met Val Leu Thr Phe Val Asn Val Ser Val His
                35             40             45
Leu Val Leu Ser Asn Phe Pro His Leu Gly Tyr Pro Cys Val Tyr Tyr
 50             55             60
His Val Val Asp Phe Glu Arg Leu Asn Met Ser Ala Tyr Asn Val Met
 65             70             75             80
His Leu His Thr Pro Met Leu Phe Leu Asp Ser Val Gln Leu Val Cys
                85             90             95
Tyr Ala Val Phe Met Gln Leu Val Phe Leu Ala Val Thr Ile Tyr Tyr
                100            105            110
Leu Val Cys Trp Ile Lys Ile Ser Met Arg Lys Asp Lys Gly Met Ser
                115            120            125
Leu Asn Gln Ser Thr Arg Asp Ile Ser Tyr Met Gly Asp Ser Leu Thr
                130            135            140
Ala Phe Leu Phe Ile Leu Ser Met Asp Thr Phe Gln Leu Phe Thr Leu
                145            150            155            160

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<400> SEQUENCE: 26

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
 1 5 10 15
 His Ser Glu Trp Asn Thr Leu Val Leu Gly Leu Leu Val Leu Ser Val
 20 25 30
 Ala Ala Ser Ser Asn Asn Thr Ser Thr Ala Ser Thr Pro Ser Pro Ser
 35 40 45
 Ser Ser Thr His Thr Ser Thr Thr Val Lys Ala Thr Thr Thr Ala Thr
 50 55 60
 Thr Ser Thr Thr Thr Ala Thr Ser Thr Thr Ser Ser Thr Thr Ser Thr
 65 70 75 80
 Lys Pro Gly Ser Thr Thr His Asp Pro Asn Val Met Arg Pro His Ala
 85 90 95
 His Asn Asp Phe Tyr Lys Ala His Cys Thr Ser His Met Tyr Glu Leu
 100 105 110
 Ser Leu Ser Ser Phe Ala Ala Trp Trp Thr Met Leu Asn Ala Leu Ile
 115 120 125
 Leu Met Gly Ala Phe Cys Ile Val Leu Arg His Cys Cys Phe Gln Asn
 130 135 140
 Phe Thr Ala Thr Thr Thr Lys Gly Tyr
 145 150

<210> SEQ ID NO 27

<211> LENGTH: 2283

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: IgE leader + gH consensus nucleic acid sequence

<400> SEQUENCE: 27

atggactgga cctggatcct gttcctggtg gccgctgcta cccgggtgca cagtcgaccc 60
 ggccctgcca gctacctgac cgtgttccgc gtgtacctgc tgagccatct gccacgccag 120
 agatacggcg ccgatgccc ctctgaggcc ctggatcctc acgacctcca tctgctgctg 180
 aacacctacg gcagacctat ccggttctg cgcgagaaca ccaccagtg cacctacaac 240
 agcagcctgc ggaacagcac cgtcgtgccc gagaatgcta tcagcttcaa cttcttccag 300
 agctacaacc agtactacgt gttccacatg ccccggtgcc tgttgccggg acctctggcc 360
 gagcagttcc tgaaccaggt ggacctgacc gagacactgg aaagatacca gcagcggctg 420
 aatacctacg cctcgtgtgc caaggacctg gccagctacc ggctcctcag ccagcagctg 480
 aaggctcagg acagcctggg cgagcagcct accaccgtgc cccctccaat cgacctgagc 540
 atcccccacg tgtggatgcc cccccagacc acacctcagc gctggaaaga gagccacacc 600
 accagcggcc tgcacagacc ccacttcaac cagacctgca ttctgttcga cggccacgac 660
 ctgctgttca gcacctgac cccctgctg caccagggct tctacctgat cgacgagctg 720
 agatacgtga agatcacct gaccgaggat ttcttctgtg tcacctgtgc catcgacgac 780
 gacaccccca tgctgctgat cttcgcccat ctgcctcggg tgctgttcaa ggccccctac 840
 cagcgggaca acttcactct gcggcagacc gagaagcacg agctgctggt gctggtcaag 900
 aaggaccagc tgaaccggca ctctacctg aaggaccccg acttctctgga cgccgcctg 960
 gacttcaact acctggacct gagcgcctg ctgagaaaca gcttccacag atacgccgtg 1020
 gacgtgctga agtccggccg gtgccagatg ctggacagac ggacctgga aatggccttc 1080
 gcctatgcc tggccctggt tgccgcccct cggcaggaag aggctggcgc tgaagtgtcc 1140

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gtgccagag ccctggacag acaggcogct ctgctgcaga tccaggaatt catgatcacc 1200
tgtctgagcc agaccccccc tcggaccacc ctgctgctgt accctaccgc cgtggatctg 1260
gccaagcggg ccctgtggac ccccaaccag atcaccgaca tcacaagcct cgtgcggtctg 1320
gtgtacatcc tgagcaagca gaaccagcag cacctgatcc cccagtgggc cctgagacag 1380
atcgccgact tcgccctgaa gctgcacaag acccacctgg ctagctttct gagcgcttc 1440
gctaggcagg aactgtacct gatgggcagc ctggtgcact ccatgctggt gcacaccacc 1500
gagaggcggg aaatcttcat cgtggaacc gccctgtgca gcctggcga gctgagccac 1560
ttcaccagc tgctggccca cccccaccac gactacctga gcgacctgta cccccctgc 1620
agctctagcg gcagacggga tcacagcctg gaacggctga cccggtggt ccccgatgcc 1680
acagtgcctg ccaactgtgc agccgcctg tccatcctgt ccaccatgca gccagcacc 1740
ctggaacct tccccgaact gttctgctg cccctggcg agagcttcag cgccctgaca 1800
gtgtccgagc acgtgtccta cgtggtcacc aaccagtacc tgatcaaggg catcagctac 1860
cccgtgtcca ccaccgtgt gggccagagc ctgatcatca cccagaccga cagccagacc 1920
aagtgcgagc tgacccggaa catgcacacc acacacagca tcaactgccg cctgaacatc 1980
agcctgaaa actgcgctt ctgccagtct gccctgctgg aatacagca taccagggc 2040
gtgatcaaca tcattgatcat gcacgacagc gacgagctgc tgttgcctt ggaccctac 2100
aacgaggtgg tgggtgccag cccccggacc cactacctga tgctgctgaa gaacggcacc 2160
gtgctggaag tgaccgacgt ggtggtggac gccaccgaca gcagactgct gatgatgagc 2220
gtgtacgccc tgagcgccat catcggcac tacctgctgt accggatgct gaaaacctgc 2280
tga 2283

```

<210> SEQ ID NO 28

<211> LENGTH: 760

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: IgE leader + gH consensus amino acid sequence

<400> SEQUENCE: 28

```

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1           5           10           15
His Ser Arg Pro Gly Leu Pro Ser Tyr Leu Thr Val Phe Ala Val Tyr
20          25          30
Leu Leu Ser His Leu Pro Ser Gln Arg Tyr Gly Ala Asp Ala Ala Ser
35          40          45
Glu Ala Leu Asp Pro His Ala Phe His Leu Leu Leu Asn Thr Tyr Gly
50          55          60
Arg Pro Ile Arg Phe Leu Arg Glu Asn Thr Thr Gln Cys Thr Tyr Asn
65          70          75          80
Ser Ser Leu Arg Asn Ser Thr Val Val Arg Glu Asn Ala Ile Ser Phe
85          90          95
Asn Phe Phe Gln Ser Tyr Asn Gln Tyr Tyr Val Phe His Met Pro Arg
100         105         110
Cys Leu Phe Ala Gly Pro Leu Ala Glu Gln Phe Leu Asn Gln Val Asp
115         120         125
Leu Thr Glu Thr Leu Glu Arg Tyr Gln Gln Arg Leu Asn Thr Tyr Ala
130         135         140
Leu Val Ser Lys Asp Leu Ala Ser Tyr Arg Ser Phe Ser Gln Gln Leu

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145		150				155				160					
Lys	Ala	Gln	Asp	Ser	Leu	Gly	Glu	Gln	Pro	Thr	Thr	Val	Pro	Pro	Pro
				165					170					175	
Ile	Asp	Leu	Ser	Ile	Pro	His	Val	Trp	Met	Pro	Pro	Gln	Thr	Thr	Pro
		180						185					190		
His	Gly	Trp	Lys	Glu	Ser	His	Thr	Thr	Ser	Gly	Leu	His	Arg	Pro	His
		195					200						205		
Phe	Asn	Gln	Thr	Cys	Ile	Leu	Phe	Asp	Gly	His	Asp	Leu	Leu	Phe	Ser
	210					215					220				
Thr	Val	Thr	Pro	Cys	Leu	His	Gln	Gly	Phe	Tyr	Leu	Ile	Asp	Glu	Leu
	225				230					235					240
Arg	Tyr	Val	Lys	Ile	Thr	Leu	Thr	Glu	Asp	Phe	Phe	Val	Val	Thr	Val
			245						250					255	
Ser	Ile	Asp	Asp	Asp	Thr	Pro	Met	Leu	Leu	Ile	Phe	Gly	His	Leu	Pro
		260						265						270	
Arg	Val	Leu	Phe	Lys	Ala	Pro	Tyr	Gln	Arg	Asp	Asn	Phe	Ile	Leu	Arg
		275					280						285		
Gln	Thr	Glu	Lys	His	Glu	Leu	Leu	Val	Leu	Val	Lys	Lys	Asp	Gln	Leu
	290					295					300				
Asn	Arg	His	Ser	Tyr	Leu	Lys	Asp	Pro	Asp	Phe	Leu	Asp	Ala	Ala	Leu
	305				310					315					320
Asp	Phe	Asn	Tyr	Leu	Asp	Leu	Ser	Ala	Leu	Leu	Arg	Asn	Ser	Phe	His
			325						330					335	
Arg	Tyr	Ala	Val	Asp	Val	Leu	Lys	Ser	Gly	Arg	Cys	Gln	Met	Leu	Asp
		340						345						350	
Arg	Arg	Thr	Val	Glu	Met	Ala	Phe	Ala	Tyr	Ala	Leu	Ala	Leu	Phe	Ala
		355					360						365		
Ala	Ala	Arg	Gln	Glu	Glu	Ala	Gly	Ala	Glu	Val	Ser	Val	Pro	Arg	Ala
	370					375					380				
Leu	Asp	Arg	Gln	Ala	Ala	Leu	Leu	Gln	Ile	Gln	Glu	Phe	Met	Ile	Thr
	385				390					395					400
Cys	Leu	Ser	Gln	Thr	Pro	Pro	Arg	Thr	Thr	Leu	Leu	Leu	Tyr	Pro	Thr
			405						410					415	
Ala	Val	Asp	Leu	Ala	Lys	Arg	Ala	Leu	Trp	Thr	Pro	Asn	Gln	Ile	Thr
		420						425						430	
Asp	Ile	Thr	Ser	Leu	Val	Arg	Leu	Val	Tyr	Ile	Leu	Ser	Lys	Gln	Asn
	435						440						445		
Gln	Gln	His	Leu	Ile	Pro	Gln	Trp	Ala	Leu	Arg	Gln	Ile	Ala	Asp	Phe
	450					455					460				
Ala	Leu	Lys	Leu	His	Lys	Thr	His	Leu	Ala	Ser	Phe	Leu	Ser	Ala	Phe
	465				470					475					480
Ala	Arg	Gln	Glu	Leu	Tyr	Leu	Met	Gly	Ser	Leu	Val	His	Ser	Met	Leu
			485						490					495	
Val	His	Thr	Thr	Glu	Arg	Arg	Glu	Ile	Phe	Ile	Val	Glu	Thr	Gly	Leu
			500					505						510	
Cys	Ser	Leu	Ala	Glu	Leu	Ser	His	Phe	Thr	Gln	Leu	Leu	Ala	His	Pro
		515						520						525	
His	His	Glu	Tyr	Leu	Ser	Asp	Leu	Tyr	Thr	Pro	Cys	Ser	Ser	Ser	Gly
	530					535					540				
Arg	Arg	Asp	His	Ser	Leu	Glu	Arg	Leu	Thr	Arg	Leu	Phe	Pro	Asp	Ala
	545				550					555					560
Thr	Val	Pro	Ala	Thr	Val	Pro	Ala	Ala	Leu	Ser	Ile	Leu	Ser	Thr	Met
				565					570					575	

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Gln Pro Ser Thr Leu Glu Thr Phe Pro Asp Leu Phe Cys Leu Pro Leu
 580 585 590
 Gly Glu Ser Phe Ser Ala Leu Thr Val Ser Glu His Val Ser Tyr Val
 595 600 605
 Val Thr Asn Gln Tyr Leu Ile Lys Gly Ile Ser Tyr Pro Val Ser Thr
 610 615 620
 Thr Val Val Gly Gln Ser Leu Ile Ile Thr Gln Thr Asp Ser Gln Thr
 625 630 635 640
 Lys Cys Glu Leu Thr Arg Asn Met His Thr Thr His Ser Ile Thr Ala
 645 650 655
 Ala Leu Asn Ile Ser Leu Glu Asn Cys Ala Phe Cys Gln Ser Ala Leu
 660 665 670
 Leu Glu Tyr Asp Asp Thr Gln Gly Val Ile Asn Ile Met Tyr Met His
 675 680 685
 Asp Ser Asp Asp Val Leu Phe Ala Leu Asp Pro Tyr Asn Glu Val Val
 690 695 700
 Val Ser Ser Pro Arg Thr His Tyr Leu Met Leu Leu Lys Asn Gly Thr
 705 710 715 720
 Val Leu Glu Val Thr Asp Val Val Val Asp Ala Thr Asp Ser Arg Leu
 725 730 735
 Leu Met Met Ser Val Tyr Ala Leu Ser Ala Ile Ile Gly Ile Tyr Leu
 740 745 750
 Leu Tyr Arg Met Leu Lys Thr Cys
 755 760

<210> SEQ ID NO 29

<211> LENGTH: 888

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: IgE leader + gL consensus nucleic acid sequence

<400> SEQUENCE: 29

```

atggattgga cctggatcct gtttctggtg gccgctgcaa caaggggtcca ctcttcagcg      60
cgccccgact gggccttcag cttcagccct ggccccgtga tcctgctgtg gtgctgctcg      120
ctgctgcccc tcgtgtcctc tgccgccgtg tctgtggccc ctacagccgc cgagaaggtg      180
ccagccgagt gccctgagct gaccagacgg tgtctgctgg gcgaggtgtt ccagggcgat      240
aagtacgaga gctggctgcg gccctggtc aacgtgaccg gcagagatgg ccccctgagc      300
cagctgatcc ggtacagacc cgtgaccctt gaggccgcca acagcgtgct gctggacgaa      360
gcctttctgg acacactggc cctgctgtac aacaaccccg accagctgcg ggccctgctg      420
aactgctga gcagcgatac cgccccaga tggatgaccg tgatgcgggg ctacagcgag      480
tgccggcagc gatctccgc cgtgtacacc tgtgtggacg acctgtgccg gggctacgac      540
ctgaccagac tgagctacgg ccggctccatc ttcacagagc acctgctggg cttcgagctg      600
gtgcccccca gcctgttcaa tgtggtggtg gccatccgga acgaggccac cgggaccaac      660
agagcagtgc ggctgctgt gtccaccgct getgetccag agggcatcac cctgtttctac      720
ggcctgtaca acgccgtgaa agagttctgc ctgagacacc agctggaccc ccccctgctg      780
cggcacctgg acaagtacta cgccggcctg cctcccagac tgaagcagac cagagtgaac      840
ctgccccccc acagcagata cggccctcag gccgtggacg ccagatga      888
  
```

<210> SEQ ID NO 30

-continued

<211> LENGTH: 295
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: IgE leader + gL consensus amino acid sequence

<400> SEQUENCE: 30

```

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1           5           10           15
His Ser Cys Arg Arg Pro Asp Cys Gly Phe Ser Phe Ser Pro Gly Pro
           20           25           30
Val Ile Leu Leu Trp Cys Cys Leu Leu Leu Pro Ile Val Ser Ser Ala
           35           40           45
Ala Val Ser Val Ala Pro Thr Ala Ala Glu Lys Val Pro Ala Glu Cys
           50           55           60
Pro Glu Leu Thr Arg Arg Cys Leu Leu Gly Glu Val Phe Gln Gly Asp
           65           70           75           80
Lys Tyr Glu Ser Trp Leu Arg Pro Leu Val Asn Val Thr Gly Arg Asp
           85           90           95
Gly Pro Leu Ser Gln Leu Ile Arg Tyr Arg Pro Val Thr Pro Glu Ala
           100          105          110
Ala Asn Ser Val Leu Leu Asp Glu Ala Phe Leu Asp Thr Leu Ala Leu
           115          120          125
Leu Tyr Asn Asn Pro Asp Gln Leu Arg Ala Leu Leu Thr Leu Leu Ser
           130          135          140
Ser Asp Thr Ala Pro Arg Trp Met Thr Val Met Arg Gly Tyr Ser Glu
           145          150          155          160
Cys Gly Asp Gly Ser Pro Ala Val Tyr Thr Cys Val Asp Asp Leu Cys
           165          170          175
Arg Gly Tyr Asp Leu Thr Arg Leu Ser Tyr Gly Arg Ser Ile Phe Thr
           180          185          190
Glu His Val Leu Gly Phe Glu Leu Val Pro Pro Ser Leu Phe Asn Val
           195          200          205
Val Val Ala Ile Arg Asn Glu Ala Thr Arg Thr Asn Arg Ala Val Arg
           210          215          220
Leu Pro Val Ser Thr Ala Ala Ala Pro Glu Gly Ile Thr Leu Phe Tyr
           225          230          235          240
Gly Leu Tyr Asn Ala Val Lys Glu Phe Cys Leu Arg His Gln Leu Asp
           245          250          255
Pro Pro Leu Leu Arg His Leu Asp Lys Tyr Tyr Ala Gly Leu Pro Pro
           260          265          270
Glu Leu Lys Gln Thr Arg Val Asn Leu Pro Ala His Ser Arg Tyr Gly
           275          280          285
Pro Gln Ala Val Asp Ala Arg
           290          295

```

<210> SEQ ID NO 31
 <211> LENGTH: 1470
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: IgE leader + gO consensus nucleic acid sequence

<400> SEQUENCE: 31

```

atggactgga cctggatcct gttcctgggc gccgctgcaa ctagagtgca cagcggcaag      60
aaagaaatga tcattggtcaa gggcatcccc aagatcatgc tgctgatcag catcaacctt      120

```

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```

ctgctgctga gcctgatcaa ctgcaacgtg ctggtcaaca gcaagggcac acggcgggagc 180
tggccctaca ccgtgctgag ctaccggggc aaagagatcc tgaagaagca gaaagaggac 240
atcctgaagc ggctgatgag caccagcagc gacggctacc ggttcctgat gtaccccagc 300
cagcagaaat tccacgccoat cgtgatcagc atggacaagt tccccagga ctacatcctg 360
gccggaccca tccggaacga cagcatcacc cacatgtggt tcgacttcta cagcaccagc 420
ctgcggaagc ccgccaata cgtgtacagc gagtacaacc acaccgcca caagatcacc 480
ctgcggcctc ccccttgogg caccgtgcc agcatgaact gcctgagcga gatgctgaac 540
gtgtccaagc ggaacgcac cggcgagaag ggctgcgga acttcaccac cttcaacccc 600
atgttcttca acgtgccccg gtggaacacc aagctgtaca tcggcagcaa caaagtgaac 660
gtggacagcc agaccatcta ctttctgggc ctgaccgccc tgctgctgcg ctacgcccag 720
agaaactgca cccggtcctt ctacctggtc aacgccatga gccggaacct gttccgggtg 780
cccaagtaca tcaacggcac caagctgaag aacaccatgc ggaagctgaa gcggaagcag 840
gccctggtca aagagcagcc ccagaagaag aacaagaagt cccagagcac caccaccccc 900
tacctgagct acaccaccag caccgccttc aacgtgacca ccaacgtgac ctacagcgcc 960
acagccgccc tgaccagagt ggccacctcc accaccggct accggcccga cagcaacttc 1020
atgaagtcca tcattggccc ccagctgagg gacctggcca cctgggtgta caccacctg 1080
cggtagacaa acgagccctt ctgcaagccc gaccggaaca gaaccgcccgt gtccgagttc 1140
atgaagaata cccacgtgct gatccgcaac gagacacct acaccatcta cggcacctg 1200
gacatgagca gcctgtacta caacgagaca atgagcgtcg agaacgagac agccagcgac 1260
aacaacgaaa ccacccccac cagccccagc acccggttcc agcggacctt catcgacccc 1320
ctgtgggact acctggacag cctgctgttc ctggacaaga tccggaactt cagcctgcag 1380
ctgcccgcct acggcaacct gacccccct gaacacagaa gggccgcca cctgagcacc 1440
ctgaacagcc tgtggtggtg gctgcagtga 1470

```

<210> SEQ ID NO 32

<211> LENGTH: 489

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: IgE leader + g0 consensus amino acid sequence

<400> SEQUENCE: 32

```

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1           5           10          15
His Ser Gly Lys Lys Glu Met Ile Met Val Lys Gly Ile Pro Lys Ile
20          25          30
Met Leu Leu Ile Ser Ile Thr Phe Leu Leu Leu Ser Leu Ile Asn Cys
35          40          45
Asn Val Leu Val Asn Ser Lys Gly Thr Arg Arg Ser Trp Pro Tyr Thr
50          55          60
Val Leu Ser Tyr Arg Gly Lys Glu Ile Leu Lys Lys Gln Lys Glu Asp
65          70          75          80
Ile Leu Lys Arg Leu Met Ser Thr Ser Ser Asp Gly Tyr Arg Phe Leu
85          90          95
Met Tyr Pro Ser Gln Gln Lys Phe His Ala Ile Val Ile Ser Met Asp
100         105         110
Lys Phe Pro Gln Asp Tyr Ile Leu Ala Gly Pro Ile Arg Asn Asp Ser
115         120         125

```

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```

Ile Thr His Met Trp Phe Asp Phe Tyr Ser Thr Gln Leu Arg Lys Pro
 130                               135                               140

Ala Lys Tyr Val Tyr Ser Glu Tyr Asn His Thr Ala His Lys Ile Thr
 145                               150                               155                               160

Leu Arg Pro Pro Pro Cys Gly Thr Val Pro Ser Met Asn Cys Leu Ser
                               165                               170                               175

Glu Met Leu Asn Val Ser Lys Arg Asn Asp Thr Gly Glu Lys Gly Cys
 180                               185                               190

Gly Asn Phe Thr Thr Phe Asn Pro Met Phe Phe Asn Val Pro Arg Trp
 195                               200                               205

Asn Thr Lys Leu Tyr Ile Gly Ser Asn Lys Val Asn Val Asp Ser Gln
 210                               215                               220

Thr Ile Tyr Phe Leu Gly Leu Thr Ala Leu Leu Leu Arg Tyr Ala Gln
 225                               230                               235                               240

Arg Asn Cys Thr Arg Ser Phe Tyr Leu Val Asn Ala Met Ser Arg Asn
 245                               250                               255

Leu Phe Arg Val Pro Lys Tyr Ile Asn Gly Thr Lys Leu Lys Asn Thr
 260                               265                               270

Met Arg Lys Leu Lys Arg Lys Gln Ala Leu Val Lys Glu Gln Pro Gln
 275                               280                               285

Lys Lys Asn Lys Lys Ser Gln Ser Thr Thr Thr Pro Tyr Leu Ser Tyr
 290                               295                               300

Thr Thr Ser Thr Ala Phe Asn Val Thr Thr Asn Val Thr Tyr Ser Ala
 305                               310                               315                               320

Thr Ala Ala Val Thr Arg Val Ala Thr Ser Thr Thr Gly Tyr Arg Pro
 325                               330                               335

Asp Ser Asn Phe Met Lys Ser Ile Met Ala Thr Gln Leu Arg Asp Leu
 340                               345                               350

Ala Thr Trp Val Tyr Thr Thr Leu Arg Tyr Arg Asn Glu Pro Phe Cys
 355                               360                               365

Lys Pro Asp Arg Asn Arg Thr Ala Val Ser Glu Phe Met Lys Asn Thr
 370                               375                               380

His Val Leu Ile Arg Asn Glu Thr Pro Tyr Thr Ile Tyr Gly Thr Leu
 385                               390                               395                               400

Asp Met Ser Ser Leu Tyr Tyr Asn Glu Thr Met Ser Val Glu Asn Glu
 405                               410                               415

Thr Ala Ser Asp Asn Asn Glu Thr Thr Pro Thr Ser Pro Ser Thr Arg
 420                               425                               430

Phe Gln Arg Thr Phe Ile Asp Pro Leu Trp Asp Tyr Leu Asp Ser Leu
 435                               440                               445

Leu Phe Leu Asp Lys Ile Arg Asn Phe Ser Leu Gln Leu Pro Ala Tyr
 450                               455                               460

Gly Asn Leu Thr Pro Pro Glu His Arg Arg Ala Ala Asn Leu Ser Thr
 465                               470                               475                               480

Leu Asn Ser Leu Trp Trp Trp Leu Gln
 485

```

<210> SEQ ID NO 33

<211> LENGTH: 567

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: IgE leader + UL128 consensus nucleic acid sequence

-continued

<400> SEQUENCE: 33

```

atggattgga cctggatcct gtttctggtg gccgctgcaa caagggtcca ctctagcccc    60
aaggatctga ccccttctct gaccgccttg tggtgctccc tgggccacag cagagtgcct    120
agagtgcggg ccgaggaatg ctgcgagttc atcaacgtga accacccccg cgagcgggtgc    180
tacgacttca agatgtgcaa ccggttcacc gtggctctga gatgccccga cggcgaagtg    240
tgctacagcc ccgagaaaac cgccgagatc cggggcatcg tgaccaccat gaccacacgc    300
ctgaccagac aggtggtgca taacaagtg accagttgca actacaaccc cctgtacctg    360
gaagccgacg gccggatcag atcgcgcaaa gtgaacgaca aggccagta cctgtggtggc    420
gtgcaggca gtgtgcctca cagatggatc aacctggaat acgacaagat caccgggatc    480
gtgggcctgg accagtacct gaaaagcgtg aagaagcaca agcggctgga cgtgtgccgg    540
gccaagatgg gctacatgct gcagtga                                         567

```

<210> SEQ ID NO 34

<211> LENGTH: 188

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: IgE leader + UL128 consensus amino acid sequence

<400> SEQUENCE: 34

```

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Thr Arg Val
 1           5           10          15
His Ser Ser Pro Lys Asp Leu Thr Pro Phe Leu Thr Ala Leu Trp Leu
          20          25          30
Leu Leu Gly His Ser Arg Val Pro Arg Val Arg Ala Glu Glu Cys Cys
          35          40          45
Glu Phe Ile Asn Val Asn His Pro Pro Glu Arg Cys Tyr Asp Phe Lys
          50          55          60
Met Cys Asn Arg Phe Thr Val Ala Leu Arg Cys Pro Asp Gly Glu Val
          65          70          75          80
Cys Tyr Ser Pro Glu Lys Thr Ala Glu Ile Arg Gly Ile Val Thr Thr
          85          90          95
Met Thr His Ser Leu Thr Arg Gln Val Val His Asn Lys Leu Thr Ser
          100         105         110
Cys Asn Tyr Asn Pro Leu Tyr Leu Glu Ala Asp Gly Arg Ile Arg Cys
          115         120         125
Gly Lys Val Asn Asp Lys Ala Gln Tyr Leu Leu Gly Ala Ala Gly Ser
          130         135         140
Val Pro Tyr Arg Trp Ile Asn Leu Glu Tyr Asp Lys Ile Thr Arg Ile
          145         150         155         160
Val Gly Leu Asp Gln Tyr Leu Glu Ser Val Lys Lys His Lys Arg Leu
          165         170         175
Asp Val Cys Arg Ala Lys Met Gly Tyr Met Leu Gln
          180         185

```

<210> SEQ ID NO 35

<211> LENGTH: 696

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: IgE leader + UL130 consensus nucleic acid sequence

<400> SEQUENCE: 35

-continued

```

atggactgga cctggatcct gttcctggtc gccgctgcta cccgggtgca cagcctgcgg    60
ctgctgctgc ggcaccactt ccaactgectg ctgctgtgtg ccgtgtgggc cacccttgt    120
ctggccagcc cttggagcac cctgaccgcc aaccagaacc ctagccccc ctggtccaag    180
ctgacctaca gcaagcccca cgacgctgct accttctact gccattcct gtaccccagc    240
cctcccagaa gccccctgca gttcagcggc ttccagcggg tgtccaccgg cctgagtgc    300
cggaacgaga cactgtacct gctgtacaac cgcgagggcc agaccctggt ggaacggtct    360
agcacctggg tcaagaaagt gatctggtat ctgagcggcc ggaaccagac catcctgcag    420
cggatgcctc ggaccgccag caagcctagc gacggcaacg tgcagatcag cgtggaagat    480
gccccaaatct tcggcgccca catggtgccc aagcagacca agctgctgag attcgtggtc    540
aacgacggca ccagatacca gatgtgctg atgaagctgg aaagctgggc ccacgtgttc    600
cgggactaca gcgtgtcatt ccaggtccga ctgaccttca ccgaggccaa caaccagacc    660
tacaccttct gcaccacccc caacctgac gtctga                                696

```

```

<210> SEQ ID NO 36
<211> LENGTH: 231
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: IgE leader + UL130 consensus amino acid
sequence

```

```

<400> SEQUENCE: 36

```

```

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Thr Arg Val
1          5          10          15

His Ser Leu Arg Leu Leu Arg His His Phe His Cys Leu Leu Leu
20          25          30

Cys Ala Val Trp Ala Thr Pro Cys Leu Ala Ser Pro Trp Ser Thr Leu
35          40          45

Thr Ala Asn Gln Asn Pro Ser Pro Pro Trp Ser Lys Leu Thr Tyr Ser
50          55          60

Lys Pro His Asp Ala Ala Thr Phe Tyr Cys Pro Phe Leu Tyr Pro Ser
65          70          75          80

Pro Pro Arg Ser Pro Leu Gln Phe Ser Gly Phe Gln Arg Val Ser Thr
85          90          95

Gly Pro Glu Cys Arg Asn Glu Thr Leu Tyr Leu Leu Tyr Asn Arg Glu
100         105         110

Gly Gln Thr Leu Val Glu Arg Ser Ser Thr Trp Val Lys Lys Val Ile
115         120         125

Trp Tyr Leu Ser Gly Arg Asn Gln Thr Ile Leu Gln Arg Met Pro Arg
130         135         140

Thr Ala Ser Lys Pro Ser Asp Gly Asn Val Gln Ile Ser Val Glu Asp
145         150         155         160

Ala Lys Ile Phe Gly Ala His Met Val Pro Lys Gln Thr Lys Leu Leu
165         170         175

Arg Phe Val Val Asn Asp Gly Thr Arg Tyr Gln Met Cys Val Met Lys
180         185         190

Leu Glu Ser Trp Ala His Val Phe Arg Asp Tyr Ser Val Ser Phe Gln
195         200         205

Val Arg Leu Thr Phe Thr Glu Ala Asn Asn Gln Thr Tyr Thr Phe Cys
210         215         220

Thr His Pro Asn Leu Ile Val

```

-continued

225

230

<210> SEQ ID NO 37
 <211> LENGTH: 438
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: IgE leader + UL131a consensus nucleic acid
 sequence

<400> SEQUENCE: 37

```

atggactgga cctggatcct gttcctggtc gccgctgcta cccgggtgca cagcagactg      60
tgcagagtgt ggctgagcgt gtgcctgtgc gccgtggtgc tgggccagtg ccagagagag      120
acagccgaga agaacgacta ctaccgggtg cccactact gggacgcctg ctctagagcc      180
ctgcccgacc agaccggta caaatcgtg gaacagctgg tggacctgac cctgaactac      240
cactacgaag ccagccaagg cctggacaac ttcgacgtgc tgaagcggat caacgtgacc      300
gaggtgtccc tgctgatcag cgacttccgg cggcagaaca gaagaggcgg caccaacaag      360
cggactacct tcaacgcgcg tggcagcctg gccctcagc ccagatccct ggaattcagc      420
gtgcggtgtg tcgccaac                                     438

```

<210> SEQ ID NO 38
 <211> LENGTH: 146
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: IgE leader + UL131a consensus amino acid
 sequence

<400> SEQUENCE: 38

```

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
 1          5          10         15
His Ser Arg Leu Cys Arg Val Trp Leu Ser Val Cys Leu Cys Ala Val
          20         25         30
Val Leu Gly Gln Cys Gln Arg Glu Thr Ala Glu Lys Asn Asp Tyr Tyr
          35         40         45
Arg Val Pro His Tyr Trp Asp Ala Cys Ser Arg Ala Leu Pro Asp Gln
          50         55         60
Thr Arg Tyr Lys Tyr Val Glu Gln Leu Val Asp Leu Thr Leu Asn Tyr
          65         70         75         80
His Tyr Asp Ala Ser His Gly Leu Asp Asn Phe Asp Val Leu Lys Arg
          85         90         95
Ile Asn Val Thr Glu Val Ser Leu Leu Ile Ser Asp Phe Arg Arg Gln
          100        105        110
Asn Arg Arg Gly Gly Thr Asn Lys Arg Thr Thr Phe Asn Ala Ala Gly
          115        120        125
Ser Leu Ala Pro His Ala Arg Ser Leu Glu Phe Ser Val Arg Leu Phe
          130        135        140
Ala Asn
145

```

<210> SEQ ID NO 39
 <211> LENGTH: 1737
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: IgE leader + UL83 consensus nucleic acid
 sequence

-continued

<400> SEQUENCE: 39

```

atggattgga cctggatcct gtttctggtg gccgctgcaa caagggtcca ctctgagagt    60
cgcgggcgga gatgccctga aatgatcagc gtgctggggc caatttccgg gcatgtgctg    120
aaggccgtct tctcccggg agacaccccc gtgctgctc acgagacaag actgctgcag    180
actggcatcc atgtgagggg ctcccagcca tctctgattc tgggtgtctca gtacacccca    240
gatagtacac cctgccacag aggggacaac cagctgcagg tgcagcatac ctacttcacc    300
ggatcagagg tcgaaaatgt gagcgtcaac gtgcacaatc ccacaggcag gagtatctgt    360
ccttcacagg agccaatgag catctacgtg tacgccctgc ccctgaaat gctgaacatc    420
cctagcatta atgtgcacca ttaccctcc gccgctgaac gaaagcaccg gcatctgcct    480
gtggcagatg ccgtcatcca tgcttcaggc aaacagatgt ggcaggcacg actgaccgtg    540
agcggactgg catggacacg acagcagaac cagtggaagg agccagacgt gtactatact    600
agcgccttcg tgttccccac caaagacgtg gccctgcgac acgtggtctg cgcacatgag    660
ctggtgtgct ctatggaaaa tactcgggcc accaagatgc aggtcattgg cgatcagtac    720
gtcaaagtgt atctggagtc cttttgtgaa gacgtgccct ctgggaagct gttcatgcac    780
gtgaccctgg gaagcgatgt cgaggaagac ctgactatga cccggaaccc acagcccttt    840
atgagacctc acgagaggaa cggttccact gtgctgtgcc caaagaatat gatcattaag    900
cccgggaaaa tctctcatat tatgctggat gtggccttta caagtccga gcatttcgga    960
ctgctgtgcc ccaaaagcat cctgggctg tcaattagcg gaaacctgct gatgaatggc   1020
cagcagatct ttctggaagt gcaggccatt cgagagaccg tcgaaactgcg acagtaacgac   1080
ccagtggcag ccctgttctt tttcgatata gacctgctgc tgcagagagg ccctcagtat   1140
agtgagcacc caacattcac ttcacagtac aggattcagg ggaagctgga gtatcggcac   1200
acttgggata gacatgacga aggagctgca cagggcgacg atgacgtgtg gacctccggc   1260
tctgatagtg acgaggaact ggtgaccaca gagcgaaaaa ctccccgggt gaccggagga   1320
ggagctatgg caggagcacc aaccagcgcc ggacgaaaga gaaaaagcgc cagcagcgcc   1380
acagcatgca ctgcaggcgt gatgacaagg gggcgctga aggcagaatc cacagtccgc   1440
cctgaggaag atactgacga ggattctgac aacgaaatcc acaatccagc cgtgttcacc   1500
tggccacctt ggcaggcagg aattctggct cgcaatctgg tccctatggt ggccactgtc   1560
caggacaga acctgaagta ccaggagttt ttctgggatg ctaatgacat ctatcggatt   1620
ttcgagagc tggaaaggcgt gtggcagcca gcagctcagc caaaaaggcg ccgacacaga   1680
caggacgcac tgctggacc atgtatgcc tccaccccaa agaaacatag gggctga    1737

```

<210> SEQ ID NO 40

<211> LENGTH: 578

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: IgE leader + UL83 consensus amino acid sequence

<400> SEQUENCE: 40

```

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Thr Arg Val
 1             5             10             15

His Ser Glu Ser Arg Gly Arg Arg Cys Pro Glu Met Ile Ser Val Leu
 20             25             30

Gly Pro Ile Ser Gly His Val Leu Lys Ala Val Phe Ser Arg Gly Asp
 35             40             45

```

-continued

Thr Pro Val Leu Pro His Glu Thr Arg Leu Leu Gln Thr Gly Ile His
 50 55 60

Val Arg Val Ser Gln Pro Ser Leu Ile Leu Val Ser Gln Tyr Thr Pro
 65 70 75 80

Asp Ser Thr Pro Cys His Arg Gly Asp Asn Gln Leu Gln Val Gln His
 85 90 95

Thr Tyr Phe Thr Gly Ser Glu Val Glu Asn Val Ser Val Asn Val His
 100 105 110

Asn Pro Thr Gly Arg Ser Ile Cys Pro Ser Gln Glu Pro Met Ser Ile
 115 120 125

Tyr Val Tyr Ala Leu Pro Leu Lys Met Leu Asn Ile Pro Ser Ile Asn
 130 135 140

Val His His Tyr Pro Ser Ala Ala Glu Arg Lys His Arg His Leu Pro
 145 150 155 160

Val Ala Asp Ala Val Ile His Ala Ser Gly Lys Gln Met Trp Gln Ala
 165 170 175

Arg Leu Thr Val Ser Gly Leu Ala Trp Thr Arg Gln Gln Asn Gln Trp
 180 185 190

Lys Glu Pro Asp Val Tyr Tyr Thr Ser Ala Phe Val Phe Pro Thr Lys
 195 200 205

Asp Val Ala Leu Arg His Val Val Cys Ala His Glu Leu Val Cys Ser
 210 215 220

Met Glu Asn Thr Arg Ala Thr Lys Met Gln Val Ile Gly Asp Gln Tyr
 225 230 235 240

Val Lys Val Tyr Leu Glu Ser Phe Cys Glu Asp Val Pro Ser Gly Lys
 245 250 255

Leu Phe Met His Val Thr Leu Gly Ser Asp Val Glu Glu Asp Leu Thr
 260 265 270

Met Thr Arg Asn Pro Gln Pro Phe Met Arg Pro His Glu Arg Asn Gly
 275 280 285

Phe Thr Val Leu Cys Pro Lys Asn Met Ile Ile Lys Pro Gly Lys Ile
 290 295 300

Ser His Ile Met Leu Asp Val Ala Phe Thr Ser His Glu His Phe Gly
 305 310 315 320

Leu Leu Cys Pro Lys Ser Ile Pro Gly Leu Ser Ile Ser Gly Asn Leu
 325 330 335

Leu Met Asn Gly Gln Gln Ile Phe Leu Glu Val Gln Ala Ile Arg Glu
 340 345 350

Thr Val Glu Leu Arg Gln Tyr Asp Pro Val Ala Ala Leu Phe Phe Phe
 355 360 365

Asp Ile Asp Leu Leu Leu Gln Arg Gly Pro Gln Tyr Ser Glu His Pro
 370 375 380

Thr Phe Thr Ser Gln Tyr Arg Ile Gln Gly Lys Leu Glu Tyr Arg His
 385 390 395 400

Thr Trp Asp Arg His Asp Glu Gly Ala Ala Gln Gly Asp Asp Asp Val
 405 410 415

Trp Thr Ser Gly Ser Asp Ser Asp Glu Glu Leu Val Thr Thr Glu Arg
 420 425 430

Lys Thr Pro Arg Val Thr Gly Gly Gly Ala Met Ala Gly Ala Ser Thr
 435 440 445

Ser Ala Gly Arg Lys Arg Lys Ser Ala Ser Ser Ala Thr Ala Cys Thr
 450 455 460

Ala Gly Val Met Thr Arg Gly Arg Leu Lys Ala Glu Ser Thr Val Ala

-continued

465	470	475	480
Pro Glu Glu Asp Thr Asp Glu Asp Ser Asp Asn Glu Ile His Asn Pro			
	485	490	495
Ala Val Phe Thr Trp Pro Pro Trp Gln Ala Gly Ile Leu Ala Arg Asn			
	500	505	510
Leu Val Pro Met Val Ala Thr Val Gln Gly Gln Asn Leu Lys Tyr Gln			
	515	520	525
Glu Phe Phe Trp Asp Ala Asn Asp Ile Tyr Arg Ile Phe Ala Glu Leu			
	530	535	540
Glu Gly Val Trp Gln Pro Ala Ala Gln Pro Lys Arg Arg Arg His Arg			
	545	550	555
Gln Asp Ala Leu Pro Gly Pro Cys Ile Ala Ser Thr Pro Lys Lys His			
	565	570	575
Arg Gly			

<210> SEQ ID NO 41

<211> LENGTH: 2802

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: IgE leader + gB consensus + HA Tag nucleic acid sequence

<400> SEQUENCE: 41

```

atggactgga cctggatcct gttcctggtg gccgctgccca cacgggtgca cagcgagagc   60
agaatctggt gcctggctgt gtgctgtaac ctgtgcatcg tgtgcctggg agccgcccgtg   120
tccagcagca gcacccgggg cacaagcgcc acacacagcc accacagcag ccacaccacc   180
agcgcggccc acagccggag cggaagcgtg agcagccagc gggtgaccag cagcgaggcc   240
gtgtcccacc gggccaacga gacaatctac aacaccaccc tgaagtacgg cgacgtcgtg   300
ggagtgaaca ccaccaagta ccctacaga gtgtgcagca tggcccaggg caccgacctg   360
atcagattcg agcggaaat cgtgtgtacc agcatgaagc ccatcaacga ggacctggac   420
gagggcatca tggtggtgta caagagaaac atcgtggccc acaccttcaa agtgcgggtg   480
taccagaagg tgetgacctt ccggcgggag tacgcctaca tccacaccac ctacctgctg   540
ggcagcaaca ccgagtagct ggcccctccc atgtgggaga tccaccacat caacagccac   600
agccagtgtc acagcagcta cagcccgctg atcgcggcca ccgtgttcgt ggccctaccac   660
cgggacagct acgagaacaa gaccatgcag ctgatgcccg acgactacag caacaccacc   720
agcaccagat acgtgaccgt gaaggaccag tggcacagcc ggggaagcac ctggctgtac   780
agagagacat gcaacctgaa ctgcatggtc accatcacca ccgccagaag caagtaccct   840
taccacttct tcgccaccag caccggcgac gtggtggaca tcagcccctt ctacaacggc   900
accaaccgga acgccagcta cttcggcgag aacgcgcgaca agttcttcat cttcccacac   960
tacaccatcg tgtccgactt cggcagaccc aacagcggcc ctgagacaca ccggctgggtg  1020
gcctttctgg aacgggcccga cagcgtgatc agctgggaca tccaggacga gaagaacctg  1080
acctgccagc tgacctctct ggaggctagc gagcggacca tcagaagcga ggccgaggac  1140
agctaccact tcagcagcgc caagatgacc gccaccttcc tgagcaagaa acaggaagtg  1200
aacatgagcg acagcgccct ggactgcgtg cgggatgagg ccatcaacaa gctgcagcag  1260
atcttcaaca ccagctacaa ccagacctac gagaagtatg gcaacgtgtc cgtgttcgag  1320
acaacaggcg gcctggtggt gttctggcag ggcacaaagc agaagtcctt ggtcagctg  1380

```

-continued

```

gaacggctgg ccaacagaag cagcctgaac ctgacccacc ggaccaagcg gagcaccgac 1440
ggcaacaata cccccacct gagcaacatg gaaagcgccc acaacctggt gtacgccag 1500
ctgcagttca cctacgacac cctgcggggc tacatcaacc gggccctggc ccagatcgcc 1560
gaggcttggt gtgtggacca gcgcgggacc ctggaagtgt tcaaagagct gagcaagatc 1620
aaccaccagc ccatcctgag cgccatctac aacaagccta tcgcccgcag attcatgggc 1680
gacgtgctgg gcctggccag ctgctgacc atcaaccaga ccagcgtgaa ggtgctgagg 1740
gacatgaaag tgaagaaag ccccggcaga tgctactcca gacctggtg catcttcaac 1800
ttcgccaaca gctcctacgt gcagtacggc cagctggggc aggacaacga gatcctgctg 1860
ggaaaccacc ggaccgagga atgccagctg cccagcctga agatctttat cgccggcaac 1920
agcgccatcg agtatgtgga ctacctgtc aagcggatga tcgacctgag cagcatcagc 1980
accgtggaca gcatgatcgc cctggacatc gacccccctg aaaacaccga cttccgggtg 2040
ctggaactgt acagccagaa agagctgagg agcagcaacg tgttcgacct ggaagagatc 2100
atgcgcgagt tcaacageta caagcagcgc gtgaaatacg tcgaggacaa ggtggtggac 2160
cccctgcccc cctacctgaa gggcctggac gacctgatga gcggcctggg agctgctggc 2220
aaggccgtgg gagtgccat tggagctgtg ggcggagccg tggccagcgt ggtggaaggc 2280
gtggccacct ttctgaagaa ccccttcggc gccttcacca tcatcctggt ggctatcgcc 2340
gtcgtgatca tcacctacct gatctacacc cggcagcggc ggctgtgtac ccagcctctg 2400
cagaacctgt tcccctacct ggtgtccgcc gacggcacca ccgtgacaag cggctccacc 2460
aaggacacca gcctgcaggc cccaccaccg tacgaggaat ccgtgtacaa cagcggcccg 2520
aagggccccag gccctcctag ctctgacgcc tctacagccg ccccacccta caccaacgag 2580
caggcctacc agatgctgct ggccttggt agactggacg ccgagcagag agcccagcag 2640
aacggaaccg acagcctgga tggccagacc ggcacccagg acaagggcca gaagcccaac 2700
ctgctggacc ggctgcggca cagaaagaac ggctaccggc acctgaagga cagcgcagaa 2760
gaggaaaaag tgtacccta cgacgtgccc gactacgctt ga 2802

```

<210> SEQ ID NO 42

<211> LENGTH: 933

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: IgE leader + gB consensus + HA Tag amino acid sequence

<400> SEQUENCE: 42

```

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1           5           10          15

```

```

His Ser Glu Ser Arg Ile Trp Cys Leu Val Val Cys Val Asn Leu Cys
20          25          30

```

```

Ile Val Cys Leu Gly Ala Ala Val Ser Ser Ser Ser Thr Arg Gly Thr
35          40          45

```

```

Ser Ala Thr His Ser His His Ser Ser His Thr Thr Ser Ala Ala His
50          55          60

```

```

Ser Arg Ser Gly Ser Val Ser Ser Gln Arg Val Thr Ser Ser Glu Ala
65          70          75          80

```

```

Val Ser His Arg Ala Asn Glu Thr Ile Tyr Asn Thr Thr Leu Lys Tyr
85          90          95

```

```

Gly Asp Val Val Gly Val Asn Thr Thr Lys Tyr Pro Tyr Arg Val Cys
100         105         110

```

-continued

Ser Met Ala Gln Gly Thr Asp Leu Ile Arg Phe Glu Arg Asn Ile Val
 115 120 125
 Cys Thr Ser Met Lys Pro Ile Asn Glu Asp Leu Asp Glu Gly Ile Met
 130 135 140
 Val Val Tyr Lys Arg Asn Ile Val Ala His Thr Phe Lys Val Arg Val
 145 150 155 160
 Tyr Gln Lys Val Leu Thr Phe Arg Arg Ser Tyr Ala Tyr Ile His Thr
 165 170 175
 Thr Tyr Leu Leu Gly Ser Asn Thr Glu Tyr Val Ala Pro Pro Met Trp
 180 185 190
 Glu Ile His His Ile Asn Ser His Ser Gln Cys Tyr Ser Ser Tyr Ser
 195 200 205
 Arg Val Ile Ala Gly Thr Val Phe Val Ala Tyr His Arg Asp Ser Tyr
 210 215 220
 Glu Asn Lys Thr Met Gln Leu Met Pro Asp Asp Tyr Ser Asn Thr His
 225 230 235 240
 Ser Thr Arg Tyr Val Thr Val Lys Asp Gln Trp His Ser Arg Gly Ser
 245 250 255
 Thr Trp Leu Tyr Arg Glu Thr Cys Asn Leu Asn Cys Met Val Thr Ile
 260 265 270
 Thr Thr Ala Arg Ser Lys Tyr Pro Tyr His Phe Phe Ala Thr Ser Thr
 275 280 285
 Gly Asp Val Val Asp Ile Ser Pro Phe Tyr Asn Gly Thr Asn Arg Asn
 290 295 300
 Ala Ser Tyr Phe Gly Glu Asn Ala Asp Lys Phe Phe Ile Phe Pro Asn
 305 310 315 320
 Tyr Thr Ile Val Ser Asp Phe Gly Arg Pro Asn Ser Ala Leu Glu Thr
 325 330 335
 His Arg Leu Val Ala Phe Leu Glu Arg Ala Asp Ser Val Ile Ser Trp
 340 345 350
 Asp Ile Gln Asp Glu Lys Asn Val Thr Cys Gln Leu Thr Phe Trp Glu
 355 360 365
 Ala Ser Glu Arg Thr Ile Arg Ser Glu Ala Glu Asp Ser Tyr His Phe
 370 375 380
 Ser Ser Ala Lys Met Thr Ala Thr Phe Leu Ser Lys Lys Gln Glu Val
 385 390 395 400
 Asn Met Ser Asp Ser Ala Leu Asp Cys Val Arg Asp Glu Ala Ile Asn
 405 410 415
 Lys Leu Gln Gln Ile Phe Asn Thr Ser Tyr Asn Gln Thr Tyr Glu Lys
 420 425 430
 Tyr Gly Asn Val Ser Val Phe Glu Thr Thr Gly Gly Leu Val Val Phe
 435 440 445
 Trp Gln Gly Ile Lys Gln Lys Ser Leu Val Glu Leu Glu Arg Leu Ala
 450 455 460
 Asn Arg Ser Ser Leu Asn Leu Thr His Arg Thr Lys Arg Ser Thr Asp
 465 470 475 480
 Gly Asn Asn Thr Thr His Leu Ser Asn Met Glu Ser Val His Asn Leu
 485 490 495
 Val Tyr Ala Gln Leu Gln Phe Thr Tyr Asp Thr Leu Arg Gly Tyr Ile
 500 505 510
 Asn Arg Ala Leu Ala Gln Ile Ala Glu Ala Trp Cys Val Asp Gln Arg
 515 520 525

-continued

Arg Thr Leu Glu Val Phe Lys Glu Leu Ser Lys Ile Asn Pro Ser Ala
 530 535 540
 Ile Leu Ser Ala Ile Tyr Asn Lys Pro Ile Ala Ala Arg Phe Met Gly
 545 550 555 560
 Asp Val Leu Gly Leu Ala Ser Cys Val Thr Ile Asn Gln Thr Ser Val
 565 570 575
 Lys Val Leu Arg Asp Met Asn Val Lys Glu Ser Pro Gly Arg Cys Tyr
 580 585 590
 Ser Arg Pro Val Val Ile Phe Asn Phe Ala Asn Ser Ser Tyr Val Gln
 595 600 605
 Tyr Gly Gln Leu Gly Glu Asp Asn Glu Ile Leu Leu Gly Asn His Arg
 610 615 620
 Thr Glu Glu Cys Gln Leu Pro Ser Leu Lys Ile Phe Ile Ala Gly Asn
 625 630 635 640
 Ser Ala Tyr Glu Tyr Val Asp Tyr Leu Phe Lys Arg Met Ile Asp Leu
 645 650 655
 Ser Ser Ile Ser Thr Val Asp Ser Met Ile Ala Leu Asp Ile Asp Pro
 660 665 670
 Leu Glu Asn Thr Asp Phe Arg Val Leu Glu Leu Tyr Ser Gln Lys Glu
 675 680 685
 Leu Arg Ser Ser Asn Val Phe Asp Leu Glu Glu Ile Met Arg Glu Phe
 690 695 700
 Asn Ser Tyr Lys Gln Arg Val Lys Tyr Val Glu Asp Lys Val Val Asp
 705 710 715 720
 Pro Leu Pro Pro Tyr Leu Lys Gly Leu Asp Asp Leu Met Ser Gly Leu
 725 730 735
 Gly Ala Ala Gly Lys Ala Val Gly Val Ala Ile Gly Ala Val Gly Gly
 740 745 750
 Ala Val Ala Ser Val Val Glu Gly Val Ala Thr Phe Leu Lys Asn Pro
 755 760 765
 Phe Gly Ala Phe Thr Ile Ile Leu Val Ala Ile Ala Val Val Ile Ile
 770 775 780
 Thr Tyr Leu Ile Tyr Thr Arg Gln Arg Arg Leu Cys Thr Gln Pro Leu
 785 790 795 800
 Gln Asn Leu Phe Pro Tyr Leu Val Ser Ala Asp Gly Thr Thr Val Thr
 805 810 815
 Ser Gly Ser Thr Lys Asp Thr Ser Leu Gln Ala Pro Pro Ser Tyr Glu
 820 825 830
 Glu Ser Val Tyr Asn Ser Gly Arg Lys Gly Pro Gly Pro Pro Ser Ser
 835 840 845
 Asp Ala Ser Thr Ala Ala Pro Pro Tyr Thr Asn Glu Gln Ala Tyr Gln
 850 855 860
 Met Leu Leu Ala Leu Ala Arg Leu Asp Ala Glu Gln Arg Ala Gln Gln
 865 870 875 880
 Asn Gly Thr Asp Ser Leu Asp Gly Gln Thr Gly Thr Gln Asp Lys Gly
 885 890 895
 Gln Lys Pro Asn Leu Leu Asp Arg Leu Arg His Arg Lys Asn Gly Tyr
 900 905 910
 Arg His Leu Lys Asp Ser Asp Glu Glu Glu Asn Val Tyr Pro Tyr Asp
 915 920 925
 Val Pro Asp Tyr Ala
 930

-continued

<210> SEQ ID NO 43
 <211> LENGTH: 1197
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: IgE leader + gM consensus + HA Tag nucleic acid sequence

<400> SEQUENCE: 43

```

atggattgga cctggatcct gttcctggtg gccgctgcta cccgggtcca cagtgcaccc    60
agccacgtgg acaaagtga caccgggact tggagcgcca gcatcgtgtt catggtgctg    120
accttcgtga atgtgtcctg ccacctggtg ctgagcaact tccccacct gggctacccc    180
tgcgtgtact accacgtggt ggacttcgag cggtgaaca tgagcgccta caacgtgatg    240
catctgcaca cccccatgct gtttctggac agcgtgcagc tcgtgtgcta cgccgtgttt    300
atgcagctgg tgttcctggc cgtgaccatc tactacctcg tgtgctggat caagatttct    360
atgcggaagg acaagggcat gagcctgaac cagagcaccg gggacatcag ctacatgggc    420
gacagcctga ccgcttctct gttcctcctg agcatggaca cttccagct gttcacctcg    480
accatgagct tccggctgcc cagcatgata gcctttatgg ccgccgtcca cttcttctgt    540
ctgaccatct tcaacgtgct catggtcacc cagtacagaa gctacaagcg gagcctgttc    600
ttcttcagtc ggctgcaccc caagctgaag ggcaccgtcc agttccggac cctgatcgtg    660
aacctggtgg aagtggcctt gggcttcaac accaccgtgg tggctatggc tctgtgctac    720
ggcttcggca acaacttctt cgtgctggca gcccacatgg tgetggcctg gttcgtggtg    780
tacgccatta tcagcatcat ctactttctg ctgatcgagg ccgtgttctt ccagtaoctg    840
aaggtgcagt tcggctacca cctggcgccc ttttctggcc tgtgctgctt gatctacccc    900
atcgtgcagt acgacacctt cctgagcaac gagtaaccga ccggcatcag ctggctcttc    960
ggcatgctgt tcttcatctg ggccatgttc accacctgtc gggccgtgctg gtacttcaga   1020
ggcagaggca gcggctcctg gaagtaccag gccctggcca cagccagcgg cgaagaagtg   1080
gccgacctga gccaccaoga cagcctggaa agcagacggc tgagagagga agaggacgac   1140
gacgacgatg aggacttoga ggacgcctac ccctacgacg tgcccgaacta tgcttga    1197

```

<210> SEQ ID NO 44
 <211> LENGTH: 398
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: IgE leader + gM consensus + HA Tag amino acid sequence

<400> SEQUENCE: 44

```

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
 1           5           10          15
His Ser Ala Pro Ser His Val Asp Lys Val Asn Thr Arg Thr Trp Ser
          20          25          30
Ala Ser Ile Val Phe Met Val Leu Thr Phe Val Asn Val Ser Val His
          35          40          45
Leu Val Leu Ser Asn Phe Pro His Leu Gly Tyr Pro Cys Val Tyr Tyr
          50          55          60
His Val Val Asp Phe Glu Arg Leu Asn Met Ser Ala Tyr Asn Val Met
          65          70          75          80
His Leu His Thr Pro Met Leu Phe Leu Asp Ser Val Gln Leu Val Cys
          85          90          95

```


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```
tggaccatgc tgaacgcct gatcctgatg ggcgccttct gcatcgtgct gggcactgc 420
tgcttcacaga acttcaccgc cacaaccacc aagggtact acccttacga tgtgcctgat 480
tatgcctga 489
```

```
<210> SEQ ID NO 46
<211> LENGTH: 162
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: IgE leader + gN consensus + HA Tag amino acid
sequence
```

```
<400> SEQUENCE: 46
```

```
Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1           5           10          15
His Ser Glu Trp Asn Thr Leu Val Leu Gly Leu Leu Val Leu Ser Val
20          25          30
Ala Ala Ser Ser Asn Asn Thr Ser Thr Ala Ser Thr Pro Ser Pro Ser
35          40          45
Ser Ser Thr His Thr Ser Thr Thr Val Lys Ala Thr Thr Thr Ala Thr
50          55          60
Thr Ser Thr Thr Thr Ala Thr Ser Thr Thr Ser Ser Thr Thr Ser Thr
65          70          75          80
Lys Pro Gly Ser Thr Thr His Asp Pro Asn Val Met Arg Pro His Ala
85          90          95
His Asn Asp Phe Tyr Lys Ala His Cys Thr Ser His Met Tyr Glu Leu
100         105         110
Ser Leu Ser Ser Phe Ala Ala Trp Trp Thr Met Leu Asn Ala Leu Ile
115         120         125
Leu Met Gly Ala Phe Cys Ile Val Leu Arg His Cys Cys Phe Gln Asn
130         135         140
Phe Thr Ala Thr Thr Thr Lys Gly Tyr Tyr Pro Tyr Asp Val Pro Asp
145         150         155         160
Tyr Ala
```

```
<210> SEQ ID NO 47
<211> LENGTH: 2310
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: IgE leader + gH consensus + HA Tag nucleic acid
sequence
```

```
<400> SEQUENCE: 47
```

```
atggactgga cctggatcct gttcctggtg gccgctgcta cccgggtgca cagtgcaccc 60
ggcctgcccc gctacctgac cgtgttgccc gtgtacctgc tgagccatct gccagccag 120
agatacggcg ccgatgcgc cctcgtaggcc ctggatcctc acgcctteca tctgtgctg 180
aacacctacg gcagacctat ccggttctcg cgcgagaaca ccaccagtg cacctacaac 240
agcagcctgc ggaacagcac cgtcgtgcgc gagaatgcta tcagcttcaa cttcttcag 300
agctacaacc agtactacgt gttccacatg ccccggtgcc tgttcgccgg acctctggcc 360
gagcagttcc tgaaccaggt ggacctgacc gagacactgg aaagatacca gcagcggctg 420
aatacctacg ccctggtgtc caaggacctg gccagctacc ggctcttcag ccagcagctg 480
aaggctcagg acagcctggg cgagcagcct accaccgtgc cccctccaat cgacctgagc 540
```

-continued

```

atcccccaag tgtggatgcc cccccagacc acacctcacg gctggaaaga gagccacacc 600
accagcggcc tgcacagacc ccacttcaac cagacctgca ttctgttcca cggccacgac 660
ctgctgttca gcaccgtgac cccctgctg caccagggct tctacctgat cgacgagctg 720
agatacgtga agatcacct gaccgaggat ttcttctgtg tcacctgtc catcgacgac 780
gacaccccc tgtgctgat ctctggccat ctgccteggg tgctgttcaa ggccccctac 840
cagcgggaca acttcactct gcggcagacc gagaagcacg agctgctggg gctggtaag 900
aaggaccagc tgaaccggca ctctacctg aaggaccccg acttctctgga cgccgcctg 960
gacttcaact acctggacct gagcgcctg ctgagaaaca gcttccacag atacgcctg 1020
gacgtgctga agtcggcgc gtgccagatg ctggacagac ggacctgga aatggcctt 1080
gcctatgccc tggccctgtt tgccgcctc cggcaggaag aggtggcgc tgaagtgtcc 1140
gtgccagag ccctggacag acaggcctc ctgctgcaga tccaggaatt catgatcacc 1200
tgtctgagcc agaccccccc tcggaccacc ctgctgctgt acctaccgc cgtggatctg 1260
gccaagcggg ccctgtggac ccccaaccag atcacgcaga tcacaagcct cgtgcccgtg 1320
gtgtacatcc tgagcaagca gaaccagcag cacctgatcc cccagtggc cctgagacag 1380
atgcgcgact tcgccctgaa gctgcacaag acccacctgg ctagcttct gagcgcctt 1440
gctaggcagg aactgtacct gatgggcagc ctggtgcact ccatgctggg gcacaccacc 1500
gagagggcgg aaatcttcat cgtggaacc ggcctgtgca gcctggccga gctgagccac 1560
ttcaccagc tgtggccca cccccaccac gagtacctga ggcacctga cccccctgc 1620
agctctagcg gcagacggga tcacagctg gaacggtga cccggtgtt cccgatgcc 1680
acagtgcctg ccactgtgcc agccgcctg tccatcctgt ccacctgca gccagcacc 1740
ctggaacct tccccgaact gttctgctg cccctgggag agagcttca cgcctgaca 1800
gtgtccgagc acgtgtccta cgtggtcacc aaccagtacc tgatcaaggg catcagctac 1860
cccgtgtcca ccaccgtct gggccagagc ctgatcatca cccagaccga cagccagacc 1920
aagtgcgagc tgacccggaa catgcacacc acacacagca tcaactgccg cctgaacatc 1980
agcctggaaa actgcccctt ctgccagtct gccctgctgg aatacgaaga taccagggc 2040
gtgatcaaca tcattgatc gcacgacagc gacgacgtgc tggtcgacct ggaccctac 2100
aacgaggtgg tgggttccag cccccggacc cactacctga tgctgctgaa gaacggcacc 2160
gtgctggaag tgaccgacgt ggtggtggac gccaccgaca gcagactgct gatgatgagc 2220
gtgtacgccc tgagcgcct catcgccatc tacctgctgt accggatgct gaaaacctgc 2280
taccctacg acgtgcccga ctacgctgga 2310

```

<210> SEQ ID NO 48

<211> LENGTH: 769

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: IgE leader + gH consensus + HA Tag amino acid sequence

<400> SEQUENCE: 48

```

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1           5           10          15

```

```

His Ser Arg Pro Gly Leu Pro Ser Tyr Leu Thr Val Phe Ala Val Tyr
20          25          30

```

```

Leu Leu Ser His Leu Pro Ser Gln Arg Tyr Gly Ala Asp Ala Ala Ser
35          40          45

```

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Glu Ala Leu Asp Pro His Ala Phe His Leu Leu Leu Asn Thr Tyr Gly
 50 55 60
 Arg Pro Ile Arg Phe Leu Arg Glu Asn Thr Thr Gln Cys Thr Tyr Asn
 65 70 75 80
 Ser Ser Leu Arg Asn Ser Thr Val Val Arg Glu Asn Ala Ile Ser Phe
 85 90 95
 Asn Phe Phe Gln Ser Tyr Asn Gln Tyr Tyr Val Phe His Met Pro Arg
 100 105 110
 Cys Leu Phe Ala Gly Pro Leu Ala Glu Gln Phe Leu Asn Gln Val Asp
 115 120 125
 Leu Thr Glu Thr Leu Glu Arg Tyr Gln Gln Arg Leu Asn Thr Tyr Ala
 130 135 140
 Leu Val Ser Lys Asp Leu Ala Ser Tyr Arg Ser Phe Ser Gln Gln Leu
 145 150 155 160
 Lys Ala Gln Asp Ser Leu Gly Glu Gln Pro Thr Thr Val Pro Pro Pro
 165 170 175
 Ile Asp Leu Ser Ile Pro His Val Trp Met Pro Pro Gln Thr Thr Pro
 180 185 190
 His Gly Trp Lys Glu Ser His Thr Thr Ser Gly Leu His Arg Pro His
 195 200 205
 Phe Asn Gln Thr Cys Ile Leu Phe Asp Gly His Asp Leu Leu Phe Ser
 210 215 220
 Thr Val Thr Pro Cys Leu His Gln Gly Phe Tyr Leu Ile Asp Glu Leu
 225 230 235 240
 Arg Tyr Val Lys Ile Thr Leu Thr Glu Asp Phe Phe Val Val Thr Val
 245 250 255
 Ser Ile Asp Asp Asp Thr Pro Met Leu Leu Ile Phe Gly His Leu Pro
 260 265 270
 Arg Val Leu Phe Lys Ala Pro Tyr Gln Arg Asp Asn Phe Ile Leu Arg
 275 280 285
 Gln Thr Glu Lys His Glu Leu Leu Val Leu Val Lys Lys Asp Gln Leu
 290 295 300
 Asn Arg His Ser Tyr Leu Lys Asp Pro Asp Phe Leu Asp Ala Ala Leu
 305 310 315 320
 Asp Phe Asn Tyr Leu Asp Leu Ser Ala Leu Leu Arg Asn Ser Phe His
 325 330 335
 Arg Tyr Ala Val Asp Val Leu Lys Ser Gly Arg Cys Gln Met Leu Asp
 340 345 350
 Arg Arg Thr Val Glu Met Ala Phe Ala Tyr Ala Leu Ala Leu Phe Ala
 355 360 365
 Ala Ala Arg Gln Glu Glu Ala Gly Ala Glu Val Ser Val Pro Arg Ala
 370 375 380
 Leu Asp Arg Gln Ala Ala Leu Leu Gln Ile Gln Glu Phe Met Ile Thr
 385 390 395 400
 Cys Leu Ser Gln Thr Pro Pro Arg Thr Thr Leu Leu Leu Tyr Pro Thr
 405 410 415
 Ala Val Asp Leu Ala Lys Arg Ala Leu Trp Thr Pro Asn Gln Ile Thr
 420 425 430
 Asp Ile Thr Ser Leu Val Arg Leu Val Tyr Ile Leu Ser Lys Gln Asn
 435 440 445
 Gln Gln His Leu Ile Pro Gln Trp Ala Leu Arg Gln Ile Ala Asp Phe
 450 455 460

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Ala Leu Lys Leu His Lys Thr His Leu Ala Ser Phe Leu Ser Ala Phe
465 470 475 480

Ala Arg Gln Glu Leu Tyr Leu Met Gly Ser Leu Val His Ser Met Leu
485 490 495

Val His Thr Thr Glu Arg Arg Glu Ile Phe Ile Val Glu Thr Gly Leu
500 505 510

Cys Ser Leu Ala Glu Leu Ser His Phe Thr Gln Leu Leu Ala His Pro
515 520 525

His His Glu Tyr Leu Ser Asp Leu Tyr Thr Pro Cys Ser Ser Ser Gly
530 535 540

Arg Arg Asp His Ser Leu Glu Arg Leu Thr Arg Leu Phe Pro Asp Ala
545 550 555 560

Thr Val Pro Ala Thr Val Pro Ala Ala Leu Ser Ile Leu Ser Thr Met
565 570 575

Gln Pro Ser Thr Leu Glu Thr Phe Pro Asp Leu Phe Cys Leu Pro Leu
580 585 590

Gly Glu Ser Phe Ser Ala Leu Thr Val Ser Glu His Val Ser Tyr Val
595 600 605

Val Thr Asn Gln Tyr Leu Ile Lys Gly Ile Ser Tyr Pro Val Ser Thr
610 615 620

Thr Val Val Gly Gln Ser Leu Ile Ile Thr Gln Thr Asp Ser Gln Thr
625 630 635 640

Lys Cys Glu Leu Thr Arg Asn Met His Thr Thr His Ser Ile Thr Ala
645 650 655

Ala Leu Asn Ile Ser Leu Glu Asn Cys Ala Phe Cys Gln Ser Ala Leu
660 665 670

Leu Glu Tyr Asp Asp Thr Gln Gly Val Ile Asn Ile Met Tyr Met His
675 680 685

Asp Ser Asp Asp Val Leu Phe Ala Leu Asp Pro Tyr Asn Glu Val Val
690 695 700

Val Ser Ser Pro Arg Thr His Tyr Leu Met Leu Leu Lys Asn Gly Thr
705 710 715 720

Val Leu Glu Val Thr Asp Val Val Val Asp Ala Thr Asp Ser Arg Leu
725 730 735

Leu Met Met Ser Val Tyr Ala Leu Ser Ala Ile Ile Gly Ile Tyr Leu
740 745 750

Leu Tyr Arg Met Leu Lys Thr Cys Tyr Pro Tyr Asp Val Pro Asp Tyr
755 760 765

Ala

<210> SEQ ID NO 49

<211> LENGTH: 915

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: IgE leader + gL consensus + HA Tag nucleic acid sequence

<400> SEQUENCE: 49

atggattgga cctggatcct gtttctggtg gccgctgcaa caaggtcca ctcttcagc 60

cggcccgact gcggttcag cttcagccct ggccccgtga tctgctgtg gtgctgcctg 120

ctgctgceca tcgtgtctc tgccgctgtg tctgtggccc ctacagccgc cgagaaggtg 180

ccagccgagt gccctgagct gaccagacgg tgtctgctgg gcgaggtgtt ccagggcgat 240

aagtacgaga gctggctgcg gccctggtc aacgtgaccg gcagagatgg cccctgagc 300

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cagctgatcc ggtacagacc cgtgaccctc gaggccgcca acagcgtgct gctggacgaa   360
gcctttctgg acacactggc cctgctgtac aacaaccccg accagctgcg ggccttctgt   420
acactgctga gcagcgatag cgcaccgaga tggatgaccg tgatgcgggg ctacagcgag   480
tgccgagcag gatctccgcg cgtgtacacc tgtgtggacg acctgtgccc gggctacgac   540
ctgaccagac tgagctacgg ccggtccatc ttcacagagc acgtgctggg ctteagctgt   600
gtgcccccca gcctgttcaa tgtggtgggt gccatccgga acgaggccac ccggaccaac   660
agagcagtgc ggctgctgtg gtcaccgctg gctgctccag agggcatcac cctgtttctc   720
ggcctgtaca acgccgtgaa agagttctgc ctgagacacc agctggaccc ccccttctgt   780
cggcacctgg acaagtacta cgcggcgctg cctcccagag tgaagcagac cagagtgaac   840
ctgcccggcc acagcagata cggccctcag gccgtggacg ccagataccc ttacgatgtg   900
cctgattatg cctga                                         915

```

<210> SEQ ID NO 50

<211> LENGTH: 304

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: IgE leader + gL Consensus + HA Tag amino acid sequence

<400> SEQUENCE: 50

```

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
 1          5          10         15
His Ser Cys Arg Arg Pro Asp Cys Gly Phe Ser Phe Ser Pro Gly Pro
          20         25         30
Val Ile Leu Leu Trp Cys Cys Leu Leu Leu Pro Ile Val Ser Ser Ala
          35         40         45
Ala Val Ser Val Ala Pro Thr Ala Ala Glu Lys Val Pro Ala Glu Cys
          50         55         60
Pro Glu Leu Thr Arg Arg Cys Leu Leu Gly Glu Val Phe Gln Gly Asp
 65         70         75         80
Lys Tyr Glu Ser Trp Leu Arg Pro Leu Val Asn Val Thr Gly Arg Asp
          85         90         95
Gly Pro Leu Ser Gln Leu Ile Arg Tyr Arg Pro Val Thr Pro Glu Ala
          100        105        110
Ala Asn Ser Val Leu Leu Asp Glu Ala Phe Leu Asp Thr Leu Ala Leu
          115        120        125
Leu Tyr Asn Asn Pro Asp Gln Leu Arg Ala Leu Leu Thr Leu Leu Ser
          130        135        140
Ser Asp Thr Ala Pro Arg Trp Met Thr Val Met Arg Gly Tyr Ser Glu
 145        150        155        160
Cys Gly Asp Gly Ser Pro Ala Val Tyr Thr Cys Val Asp Asp Leu Cys
          165        170        175
Arg Gly Tyr Asp Leu Thr Arg Leu Ser Tyr Gly Arg Ser Ile Phe Thr
          180        185        190
Glu His Val Leu Gly Phe Glu Leu Val Pro Pro Ser Leu Phe Asn Val
          195        200        205
Val Val Ala Ile Arg Asn Glu Ala Thr Arg Thr Asn Arg Ala Val Arg
          210        215        220
Leu Pro Val Ser Thr Ala Ala Ala Pro Glu Gly Ile Thr Leu Phe Tyr
 225        230        235        240

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-continued

Gly Leu Tyr Asn Ala Val Lys Glu Phe Cys Leu Arg His Gln Leu Asp
 245 250 255

Pro Pro Leu Leu Arg His Leu Asp Lys Tyr Tyr Ala Gly Leu Pro Pro
 260 265 270

Glu Leu Lys Gln Thr Arg Val Asn Leu Pro Ala His Ser Arg Tyr Gly
 275 280 285

Pro Gln Ala Val Asp Ala Arg Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
 290 295 300

<210> SEQ ID NO 51
 <211> LENGTH: 1497
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: IgE leader + gO consensus + HA Tag nucleic acid
 sequence

<400> SEQUENCE: 51

atggactgga cctggatcct gttcctggtc gccgctgcaa ctagagtgca cagcggcaag 60
 aaagaaatga tcattggtcaa gggcatcccc aagatcatgc tgctgatcag catcaccttt 120
 ctgctgctga gcctgatcaa ctgcaacgtg ctggccaaca gcaagggcac acggcggagc 180
 tggccctaca ccgtgctgag ctaccggggc aaagagatcc tgaagaagca gaaagaggac 240
 atcctgaagc ggctgatgag caccagcagc gacggctacc ggctcctgat gtaccccagc 300
 cagcagaaat tccacgccaat cgtgatcagc atggacaagt tccccagga ctacatcctg 360
 gccggaccca tccggaacga cagcatcacc cacatgtggt tcgacttcta cagcaaccag 420
 ctgcggaagc ccgccaataa cgtgtacagc gagtacaacc acaccgcca caagatcacc 480
 ctgcggcctc ccccttgogg caccgtgcc agcatgaact gcctgagcga gatgctgaac 540
 gtgtccaagc ggaacgacac cggcgagaag ggctgcggca acttcaccac ctccaacccc 600
 atgttcttca acgtgccccg gtggaacacc aagctgtaca tcggcagcaa caaagtgaac 660
 gtggacagcc agaccatcta ctttctgggc ctgaccgccc tgctgctgcg ctacgcccag 720
 agaaactgca cccggctcct ctacctggtc aacgccatga gccggaacct gttccgggtg 780
 cccaagtaca tcaacggcac caagctgaag aacaccatgc ggaagctgaa gcggaagcag 840
 gccctggtca aagagcagcc ccagaagaag aacaagaagt cccagagcac caccaccccc 900
 tacctgagct acaccaccag caccgccttc aacgtgacca ccaacgtgac ctacagcgcc 960
 acagccgccc tgaccagagt ggccacctcc accaccggct accggcccga cagcaacttc 1020
 atgaagtcca tcattggccc ccagctgagg gacctggcca cctgggtgta caccacctg 1080
 cggtagacaa acgagccctt ctgcaagccc gaccggaaca gaaccgcccgt gtccgagttc 1140
 atgaagaata cccacgtgct gatccgcaac gagacacct acaccatcta cggcaccctg 1200
 gacatgagca gcctgtacta caacgagaca atgagcgtcg agaacgagac agccagcgac 1260
 aacaacgaaa ccacccccac cagccccagc acccggttcc agcggacctt catcgacccc 1320
 ctgtgggact acctggacag cctgctgttc ctggacaaga tccggaactt cagcctgcag 1380
 ctgcccgcct acggcaacct gacccccctt gaacacagaa gggccgcca cctgagcacc 1440
 ctgaacagcc tgtggtggtg gctgcagtac ccctacgacg tgcccgacta cgcctga 1497

<210> SEQ ID NO 52
 <211> LENGTH: 498
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:

-continued

 <223> OTHER INFORMATION: IgE leader + g0 consensus + HA Tag amino acid sequence

<400> SEQUENCE: 52

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
 1 5 10 15
 His Ser Gly Lys Lys Glu Met Ile Met Val Lys Gly Ile Pro Lys Ile
 20 25 30
 Met Leu Leu Ile Ser Ile Thr Phe Leu Leu Leu Ser Leu Ile Asn Cys
 35 40 45
 Asn Val Leu Val Asn Ser Lys Gly Thr Arg Arg Ser Trp Pro Tyr Thr
 50 55 60
 Val Leu Ser Tyr Arg Gly Lys Glu Ile Leu Lys Lys Gln Lys Glu Asp
 65 70 75 80
 Ile Leu Lys Arg Leu Met Ser Thr Ser Ser Asp Gly Tyr Arg Phe Leu
 85 90 95
 Met Tyr Pro Ser Gln Gln Lys Phe His Ala Ile Val Ile Ser Met Asp
 100 105 110
 Lys Phe Pro Gln Asp Tyr Ile Leu Ala Gly Pro Ile Arg Asn Asp Ser
 115 120 125
 Ile Thr His Met Trp Phe Asp Phe Tyr Ser Thr Gln Leu Arg Lys Pro
 130 135 140
 Ala Lys Tyr Val Tyr Ser Glu Tyr Asn His Thr Ala His Lys Ile Thr
 145 150 155 160
 Leu Arg Pro Pro Pro Cys Gly Thr Val Pro Ser Met Asn Cys Leu Ser
 165 170 175
 Glu Met Leu Asn Val Ser Lys Arg Asn Asp Thr Gly Glu Lys Gly Cys
 180 185 190
 Gly Asn Phe Thr Thr Phe Asn Pro Met Phe Phe Asn Val Pro Arg Trp
 195 200 205
 Asn Thr Lys Leu Tyr Ile Gly Ser Asn Lys Val Asn Val Asp Ser Gln
 210 215 220
 Thr Ile Tyr Phe Leu Gly Leu Thr Ala Leu Leu Leu Arg Tyr Ala Gln
 225 230 235 240
 Arg Asn Cys Thr Arg Ser Phe Tyr Leu Val Asn Ala Met Ser Arg Asn
 245 250 255
 Leu Phe Arg Val Pro Lys Tyr Ile Asn Gly Thr Lys Leu Lys Asn Thr
 260 265 270
 Met Arg Lys Leu Lys Arg Lys Gln Ala Leu Val Lys Glu Gln Pro Gln
 275 280 285
 Lys Lys Asn Lys Lys Ser Gln Ser Thr Thr Thr Pro Tyr Leu Ser Tyr
 290 295 300
 Thr Thr Ser Thr Ala Phe Asn Val Thr Thr Asn Val Thr Tyr Ser Ala
 305 310 315 320
 Thr Ala Ala Val Thr Arg Val Ala Thr Ser Thr Thr Gly Tyr Arg Pro
 325 330 335
 Asp Ser Asn Phe Met Lys Ser Ile Met Ala Thr Gln Leu Arg Asp Leu
 340 345 350
 Ala Thr Trp Val Tyr Thr Thr Leu Arg Tyr Arg Asn Glu Pro Phe Cys
 355 360 365
 Lys Pro Asp Arg Asn Arg Thr Ala Val Ser Glu Phe Met Lys Asn Thr
 370 375 380
 His Val Leu Ile Arg Asn Glu Thr Pro Tyr Thr Ile Tyr Gly Thr Leu
 385 390 395 400

-continued

Asp Met Ser Ser Leu Tyr Tyr Asn Glu Thr Met Ser Val Glu Asn Glu
 405 410 415

Thr Ala Ser Asp Asn Asn Glu Thr Thr Pro Thr Ser Pro Ser Thr Arg
 420 425 430

Phe Gln Arg Thr Phe Ile Asp Pro Leu Trp Asp Tyr Leu Asp Ser Leu
 435 440 445

Leu Phe Leu Asp Lys Ile Arg Asn Phe Ser Leu Gln Leu Pro Ala Tyr
 450 455 460

Gly Asn Leu Thr Pro Pro Glu His Arg Arg Ala Ala Asn Leu Ser Thr
 465 470 475 480

Leu Asn Ser Leu Trp Trp Trp Leu Gln Tyr Pro Tyr Asp Val Pro Asp
 485 490 495

Tyr Ala

<210> SEQ ID NO 53
 <211> LENGTH: 594
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: IgE leader + UL128 consensus + HA Tag nucleic
 acid sequence

<400> SEQUENCE: 53

atggattgga cctggatcct gtttctggtg gccgctgcaa caagggtcca ctctagcccc 60
 aaggatctga ccccttctct gaccgcoctg tggetgctcc tgggccacag cagagtgcct 120
 agagtgcggg ccgaggaatg ctgagagttc atcaacgtga accaccccc cgagcgggtgc 180
 tacgacttca agatgtgcaa ccgggtcacc gtggctctga gatgccccga cggcgaagtg 240
 tgctacagcc ccgagaaaac cgccgagatc cggggcatcg tgaccaccat gaccacacagc 300
 ctgaccagac aggtggtgca taacaagctg accagttgca actacaaccc cctgtactctg 360
 gaagccgacg gccggatcag atcgcgcaaa gtgaacgaca aggcccagta cctgctggggc 420
 gctgcaggca gtgtgcctca cagatggatc aacctggaat acgacaagat caccgggatc 480
 gtgggcctgg accagtacct gaaaagcgtg aagaagcaca agcggctgga cgtgtgccgg 540
 gccaaagtgg gctacatgct gcagtagcca tatgacgtcc ccgattacgc ttga 594

<210> SEQ ID NO 54
 <211> LENGTH: 197
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: IgE leader + UL128 consensus + HA Tag amino
 acid sequence

<400> SEQUENCE: 54

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
 1 5 10 15

His Ser Ser Pro Lys Asp Leu Thr Pro Phe Leu Thr Ala Leu Trp Leu
 20 25 30

Leu Leu Gly His Ser Arg Val Pro Arg Val Arg Ala Glu Glu Cys Cys
 35 40 45

Glu Phe Ile Asn Val Asn His Pro Pro Glu Arg Cys Tyr Asp Phe Lys
 50 55 60

Met Cys Asn Arg Phe Thr Val Ala Leu Arg Cys Pro Asp Gly Glu Val
 65 70 75 80

Cys Tyr Ser Pro Glu Lys Thr Ala Glu Ile Arg Gly Ile Val Thr Thr

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85					90					95					
Met	Thr	His	Ser	Leu	Thr	Arg	Gln	Val	Val	His	Asn	Lys	Leu	Thr	Ser
			100					105					110		
Cys	Asn	Tyr	Asn	Pro	Leu	Tyr	Leu	Glu	Ala	Asp	Gly	Arg	Ile	Arg	Cys
		115					120					125			
Gly	Lys	Val	Asn	Asp	Lys	Ala	Gln	Tyr	Leu	Leu	Gly	Ala	Ala	Gly	Ser
	130					135					140				
Val	Pro	Tyr	Arg	Trp	Ile	Asn	Leu	Glu	Tyr	Asp	Lys	Ile	Thr	Arg	Ile
145						150					155				160
Val	Gly	Leu	Asp	Gln	Tyr	Leu	Glu	Ser	Val	Lys	Lys	His	Lys	Arg	Leu
			165						170					175	
Asp	Val	Cys	Arg	Ala	Lys	Met	Gly	Tyr	Met	Leu	Gln	Tyr	Pro	Tyr	Asp
			180					185						190	
Val	Pro	Asp	Tyr	Ala											
			195												

<210> SEQ ID NO 55

<211> LENGTH: 723

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: IgE leader + UL130 consensus + HA Tag nucleic acid sequence

<400> SEQUENCE: 55

```

atggactgga cctggatcct gttcctggtc gccgctgcta cccgggtgca cagcctgceg      60
ctgctgctgc ggcaccactt ccactgcctg ctgctgtgtg ccgtgtgggc cacccttgt      120
ctggccagcc cttggagcac cctgaccgcc aaccagaacc ctagcccccc ctggtccaag      180
ctgacctaca gcaagcccca cgacgcoget accttctact gcccattcct gtaccccgag      240
cctcccagaa gccccctgca gttcagcggc ttccagcggg tgtccaccgg cctgagtg      300
cggaacgaga cactgtacct gctgtacaac cgcgagggcc agaccctggt ggaacggtct      360
agcacctggg tcaagaaagt gatctggtat ctgagcggcc ggaaccagac catcctgcag      420
cggatgcctc ggaccgccag caagcctagc gacggcaacg tgcagatcag cgtggaagat      480
gccaaaatct tcggcgccca catggtgccc aagcagacca agctgctgag attcgtggtc      540
aacgacggca ccagatacca gatgtgcgtg atgaagctgg aaagctgggc ccacgtgttc      600
cgggactaca gcgtgtcatt ccaggtccga ctgaccttca ccgaggccaa caaccagacc      660
tacaccttct gcacccaccc caacctgatc gtctaccctt acgacgtgcc agattatgcc      720
tga                                                                                   723

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<210> SEQ ID NO 56

<211> LENGTH: 240

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: IgE leader + UL130 consensus + HA Tag amino acid sequence

<400> SEQUENCE: 56

Met	Asp	Trp	Thr	Trp	Ile	Leu	Phe	Leu	Val	Ala	Ala	Ala	Thr	Arg	Val
1			5						10					15	
His	Ser	Leu	Arg	Leu	Leu	Leu	Arg	His	His	Phe	His	Cys	Leu	Leu	Leu
		20					25					30			
Cys	Ala	Val	Trp	Ala	Thr	Pro	Cys	Leu	Ala	Ser	Pro	Trp	Ser	Thr	Leu
		35					40					45			

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Thr Ala Asn Gln Asn Pro Ser Pro Pro Trp Ser Lys Leu Thr Tyr Ser
 50 55 60
 Lys Pro His Asp Ala Ala Thr Phe Tyr Cys Pro Phe Leu Tyr Pro Ser
 65 70 75 80
 Pro Pro Arg Ser Pro Leu Gln Phe Ser Gly Phe Gln Arg Val Ser Thr
 85 90 95
 Gly Pro Glu Cys Arg Asn Glu Thr Leu Tyr Leu Leu Tyr Asn Arg Glu
 100 105 110
 Gly Gln Thr Leu Val Glu Arg Ser Ser Thr Trp Val Lys Lys Val Ile
 115 120 125
 Trp Tyr Leu Ser Gly Arg Asn Gln Thr Ile Leu Gln Arg Met Pro Arg
 130 135 140
 Thr Ala Ser Lys Pro Ser Asp Gly Asn Val Gln Ile Ser Val Glu Asp
 145 150 155 160
 Ala Lys Ile Phe Gly Ala His Met Val Pro Lys Gln Thr Lys Leu Leu
 165 170 175
 Arg Phe Val Val Asn Asp Gly Thr Arg Tyr Gln Met Cys Val Met Lys
 180 185 190
 Leu Glu Ser Trp Ala His Val Phe Arg Asp Tyr Ser Val Ser Phe Gln
 195 200 205
 Val Arg Leu Thr Phe Thr Glu Ala Asn Asn Gln Thr Tyr Thr Phe Cys
 210 215 220
 Thr His Pro Asn Leu Ile Val Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
 225 230 235 240

<210> SEQ ID NO 57

<211> LENGTH: 468

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: IgE leader + UL131a consensus + HA Tag nucleic acid sequence

<400> SEQUENCE: 57

atggactgga cctggatcct gttcctggtc gccgctgcta cccgggtgca cagcagactg 60
 tgcagagtgt ggctgagcgt gtcctgtgtc gccgtggtgc tgggccagtgc ccagagagag 120
 acagccgaga agaacgacta ctaccgggtg cccactact gggacgcctg ctctagagcc 180
 ctgcccgacc agaccggta caaatacgtg gaacagctgg tggacctgac cctgaactac 240
 cactacgacg ccagccacgg cctggacaac ttcgacgtgc tgaagcggat caactgac 300
 gaggtgtccc tgctgatcag cgacttcgg cggcagaaca gaagaggcgg caccaacaag 360
 cggactacct tcaacgcgcg tggcagcctg gccctcag ccagatccct ggaattcagc 420
 gtgcggctgt tcgccaacta tccgtacgac gtcccagact acgctga 468

<210> SEQ ID NO 58

<211> LENGTH: 155

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: IgE leader + UL131a consensus + HA Tag amino acid sequence

<400> SEQUENCE: 58

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
 1 5 10 15
 His Ser Arg Leu Cys Arg Val Trp Leu Ser Val Cys Leu Cys Ala Val

-continued

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tctgatagtg acgaggaact ggtgaccaca gagcgaaaaa ctccccgggt gaccggagga 1320
ggagctatgg caggagcatc aaccagcgcc ggacgaaaga gaaaaagcgc cagcagcgcc 1380
acagcatgca ctgcaggcgt gatgacaagg gggcgctga aggcagaatc cacagtgcgc 1440
cctgaggaag atactgacga ggattctgac aacgaaatcc acaatccagc cgtgttcacc 1500
tggccacctt ggcaggcagg aattctggct cgcaatctgg tccctatggt ggccactgtc 1560
cagggacaga acctgaagta ccaggagttt ttctgggatg ctaatgacat ctatcggatt 1620
ttcgcagagc tggaaggcgt gtggcagcca gcagctcagc caaaaaggcg ccgacacaga 1680
caggacgcac tgcttgacc atgtatcgcc tccaccccaa agaaacatag gggctaccct 1740
tacgatgtgc ctgattatgc ctga 1764

```

```

<210> SEQ ID NO 60
<211> LENGTH: 587
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: IgE leader + UL83 consensus + HA Tag amino acid
sequence

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<400> SEQUENCE: 60

```

```

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1          5          10         15
His Ser Glu Ser Arg Gly Arg Arg Cys Pro Glu Met Ile Ser Val Leu
20        25        30
Gly Pro Ile Ser Gly His Val Leu Lys Ala Val Phe Ser Arg Gly Asp
35        40        45
Thr Pro Val Leu Pro His Glu Thr Arg Leu Leu Gln Thr Gly Ile His
50        55        60
Val Arg Val Ser Gln Pro Ser Leu Ile Leu Val Ser Gln Tyr Thr Pro
65        70        75        80
Asp Ser Thr Pro Cys His Arg Gly Asp Asn Gln Leu Gln Val Gln His
85        90        95
Thr Tyr Phe Thr Gly Ser Glu Val Glu Asn Val Ser Val Asn Val His
100       105       110
Asn Pro Thr Gly Arg Ser Ile Cys Pro Ser Gln Glu Pro Met Ser Ile
115       120       125
Tyr Val Tyr Ala Leu Pro Leu Lys Met Leu Asn Ile Pro Ser Ile Asn
130       135       140
Val His His Tyr Pro Ser Ala Ala Glu Arg Lys His Arg His Leu Pro
145       150       155       160
Val Ala Asp Ala Val Ile His Ala Ser Gly Lys Gln Met Trp Gln Ala
165       170       175
Arg Leu Thr Val Ser Gly Leu Ala Trp Thr Arg Gln Gln Asn Gln Trp
180       185       190
Lys Glu Pro Asp Val Tyr Tyr Thr Ser Ala Phe Val Phe Pro Thr Lys
195       200       205
Asp Val Ala Leu Arg His Val Val Cys Ala His Glu Leu Val Cys Ser
210       215       220
Met Glu Asn Thr Arg Ala Thr Lys Met Gln Val Ile Gly Asp Gln Tyr
225       230       235       240
Val Lys Val Tyr Leu Glu Ser Phe Cys Glu Asp Val Pro Ser Gly Lys
245       250       255
Leu Phe Met His Val Thr Leu Gly Ser Asp Val Glu Glu Asp Leu Thr
260       265       270

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Met Thr Arg Asn Pro Gln Pro Phe Met Arg Pro His Glu Arg Asn Gly
 275 280 285

Phe Thr Val Leu Cys Pro Lys Asn Met Ile Ile Lys Pro Gly Lys Ile
 290 295 300

Ser His Ile Met Leu Asp Val Ala Phe Thr Ser His Glu His Phe Gly
 305 310 315 320

Leu Leu Cys Pro Lys Ser Ile Pro Gly Leu Ser Ile Ser Gly Asn Leu
 325 330 335

Leu Met Asn Gly Gln Gln Ile Phe Leu Glu Val Gln Ala Ile Arg Glu
 340 345 350

Thr Val Glu Leu Arg Gln Tyr Asp Pro Val Ala Ala Leu Phe Phe Phe
 355 360 365

Asp Ile Asp Leu Leu Leu Gln Arg Gly Pro Gln Tyr Ser Glu His Pro
 370 375 380

Thr Phe Thr Ser Gln Tyr Arg Ile Gln Gly Lys Leu Glu Tyr Arg His
 385 390 395 400

Thr Trp Asp Arg His Asp Glu Gly Ala Ala Gln Gly Asp Asp Asp Val
 405 410 415

Trp Thr Ser Gly Ser Asp Ser Asp Glu Glu Leu Val Thr Thr Glu Arg
 420 425 430

Lys Thr Pro Arg Val Thr Gly Gly Gly Ala Met Ala Gly Ala Ser Thr
 435 440 445

Ser Ala Gly Arg Lys Arg Lys Ser Ala Ser Ser Ala Thr Ala Cys Thr
 450 455 460

Ala Gly Val Met Thr Arg Gly Arg Leu Lys Ala Glu Ser Thr Val Ala
 465 470 475 480

Pro Glu Glu Asp Thr Asp Glu Asp Ser Asp Asn Glu Ile His Asn Pro
 485 490 495

Ala Val Phe Thr Trp Pro Pro Trp Gln Ala Gly Ile Leu Ala Arg Asn
 500 505 510

Leu Val Pro Met Val Ala Thr Val Gln Gly Gln Asn Leu Lys Tyr Gln
 515 520 525

Glu Phe Phe Trp Asp Ala Asn Asp Ile Tyr Arg Ile Phe Ala Glu Leu
 530 535 540

Glu Gly Val Trp Gln Pro Ala Ala Gln Pro Lys Arg Arg Arg His Arg
 545 550 555 560

Gln Asp Ala Leu Pro Gly Pro Cys Ile Ala Ser Thr Pro Lys Lys His
 565 570 575

Arg Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
 580 585

<210> SEQ ID NO 61
 <211> LENGTH: 18
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: IgE leader amino acid sequence

<400> SEQUENCE: 61

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
 1 5 10 15

His Ser

<210> SEQ ID NO 62
 <211> LENGTH: 9

-continued

<212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: HA Tag amino acid sequence

<400> SEQUENCE: 62

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
 1 5

<210> SEQ ID NO 63
 <211> LENGTH: 7
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Furin protease cleavage site amino acid
 sequence

<400> SEQUENCE: 63

Arg Gly Arg Lys Arg Arg Ser
 1 5

<210> SEQ ID NO 64
 <211> LENGTH: 1650
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Plasmid 2 insert - IgE leader + gM consensus +
 HA Tag + Furin + gN consensus - HA Tag nucleic acid sequence

<400> SEQUENCE: 64

atggattgga cctggatcct gttcctggtg gccgctgcta cccgggtcca cagtgcaccc 60
 agccacgtgg acaaaagtga cccccggact tggagcgcca gcatcgtgtt catggtgctg 120
 accttcgtga atgtgtccgt ccacctggtg ctgagcaact tccccacctt gggtaacccc 180
 tgcgtgtact accacgtggt ggacttcgag cggctgaaca tgagcgcta caacgtgatg 240
 catctgcaca ccccatgct gtttctggac agcgtgcagc tcgtgtgcta cgccgtgttt 300
 atgcagctgg tgttcctggc cgtgaccatc tactacctcg tgtgctggat caagatttct 360
 atgcggaagg acaagggcat gagcctgaac cagagcacc cggacatcag ctacatgggc 420
 gacagcctga ccgcttctct gttcatctct agcatggaca ccttcagct gttcacctctg 480
 accatgagct tccggctgcc cagcatgatc gcctttatgg ccgccgtcca cttcttctgt 540
 ctgaccatct tcaacgtgtc catggtcacc cagtacagaa gctacaagcg gagcctgttc 600
 ttcttcagtc ggctgcaccc caagctgaag ggcaccgtcc agttccggac cctgatcgtg 660
 aacctggtgg aagtggccct gggcttcaac accaccgtgg tggctatggc tctgtgetac 720
 ggcttcggca acaacttctt cgtgctggaca ggccacatgg tgctggccgt gttcgtgggtg 780
 tacgccatta tcagcatcat ctactttctg ctgatcgagg ccgtgttctt ccagtacgtg 840
 aaggtgcagt tcggtacca cctggcgccc ttttctggcc tgtgcccct gatctaaccc 900
 atcgtgcagt acgacacctt cctgagcaac gagtaccgga ccggcatcag ctggtccttc 960
 ggcatgctgt tctcatctg ggccatgttc accacctgtc gggccgtgcg gtacttcaga 1020
 ggagagggca gggctcctg gaagtaaccag gccctggcca cagccagcgg cgaagaagtg 1080
 gccgacctga gccaccacga cagcctggaa agcagacggc tgagagagga agaggacgac 1140
 gacgacgatg aggacttoga ggacgcctac ccctacgacg tgcccgaacta tgcccggggc 1200
 agaaagcggg gatctgagtg gaacacctg gtgctgggtc tgctggtgct gtctgtggcc 1260
 gccagcagca acaacaccag cactgccagc acccccagcc ctagcagcag caccacaccc 1320

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tccaccacg tgaaggccac caccaccgcc accacaagca ccacaacagc caccagcacc 1380
acctttcca ccaccagcac aaagcccggc agcaccactc acgaccccaa cgtgatgagg 1440
ccccagccc acaacgactt ctacaaggcc cactgcacca gccatatgta cgagctgagc 1500
ctgagcagct tcgccgctg gtggaccatg ctgaacgccc tgatcctgat gggcgcttc 1560
tgcacgtgctg tgcggcactg ctgcttcag aacttcaccg ccacaaccac caagggtac 1620
tacccttagc atgtgcctga ttatgcctga 1650

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<210> SEQ ID NO 65

<211> LENGTH: 549

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

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<223> OTHER INFORMATION: Plasmid 2 amino acid sequence - IgE leader + gM
consensus + HA Tag + Furin + gN consensus + HA Tag amino acid
sequence

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<400> SEQUENCE: 65

```

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1           5           10           15
His Ser Ala Pro Ser His Val Asp Lys Val Asn Thr Arg Thr Trp Ser
20           25           30
Ala Ser Ile Val Phe Met Val Leu Thr Phe Val Asn Val Ser Val His
35           40           45
Leu Val Leu Ser Asn Phe Pro His Leu Gly Tyr Pro Cys Val Tyr Tyr
50           55           60
His Val Val Asp Phe Glu Arg Leu Asn Met Ser Ala Tyr Asn Val Met
65           70           75           80
His Leu His Thr Pro Met Leu Phe Leu Asp Ser Val Gln Leu Val Cys
85           90           95
Tyr Ala Val Phe Met Gln Leu Val Phe Leu Ala Val Thr Ile Tyr Tyr
100          105          110
Leu Val Cys Trp Ile Lys Ile Ser Met Arg Lys Asp Lys Gly Met Ser
115          120          125
Leu Asn Gln Ser Thr Arg Asp Ile Ser Tyr Met Gly Asp Ser Leu Thr
130          135          140
Ala Phe Leu Phe Ile Leu Ser Met Asp Thr Phe Gln Leu Phe Thr Leu
145          150          155          160
Thr Met Ser Phe Arg Leu Pro Ser Met Ile Ala Phe Met Ala Ala Val
165          170          175
His Phe Phe Cys Leu Thr Ile Phe Asn Val Ser Met Val Thr Gln Tyr
180          185          190
Arg Ser Tyr Lys Arg Ser Leu Phe Phe Phe Ser Arg Leu His Pro Lys
195          200          205
Leu Lys Gly Thr Val Gln Phe Arg Thr Leu Ile Val Asn Leu Val Glu
210          215          220
Val Ala Leu Gly Phe Asn Thr Thr Val Val Ala Met Ala Leu Cys Tyr
225          230          235          240
Gly Phe Gly Asn Asn Phe Phe Val Arg Thr Gly His Met Val Leu Ala
245          250          255
Val Phe Val Val Tyr Ala Ile Ile Ser Ile Ile Tyr Phe Leu Leu Ile
260          265          270
Glu Ala Val Phe Phe Gln Tyr Val Lys Val Gln Phe Gly Tyr His Leu
275          280          285
Gly Ala Phe Phe Gly Leu Cys Gly Leu Ile Tyr Pro Ile Val Gln Tyr

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290			295			300									
Asp	Thr	Phe	Leu	Ser	Asn	Glu	Tyr	Arg	Thr	Gly	Ile	Ser	Trp	Ser	Phe
305					310					315					320
Gly	Met	Leu	Phe	Phe	Ile	Trp	Ala	Met	Phe	Thr	Thr	Cys	Arg	Ala	Val
				325						330					335
Arg	Tyr	Phe	Arg	Gly	Arg	Gly	Ser	Gly	Ser	Val	Lys	Tyr	Gln	Ala	Leu
			340							345					350
Ala	Thr	Ala	Ser	Gly	Glu	Glu	Val	Ala	Ala	Leu	Ser	His	His	Asp	Ser
		355								360					365
Leu	Glu	Ser	Arg	Arg	Leu	Arg	Glu	Glu	Glu	Asp	Asp	Asp	Asp	Asp	Glu
	370						375								380
Asp	Phe	Glu	Asp	Ala	Tyr	Pro	Tyr	Asp	Val	Pro	Asp	Tyr	Ala	Arg	Gly
385					390						395				400
Arg	Lys	Arg	Arg	Ser	Glu	Trp	Asn	Thr	Leu	Val	Leu	Gly	Leu	Leu	Val
				405						410					415
Leu	Ser	Val	Ala	Ala	Ser	Ser	Asn	Asn	Thr	Ser	Thr	Ala	Ser	Thr	Pro
			420							425					430
Ser	Pro	Ser	Ser	Ser	Thr	His	Thr	Ser	Thr	Thr	Val	Lys	Ala	Thr	Thr
		435								440					445
Thr	Ala	Thr	Thr	Ser	Thr	Thr	Thr	Ala	Thr	Ser	Thr	Thr	Ser	Ser	Thr
	450														460
Thr	Ser	Thr	Lys	Pro	Gly	Ser	Thr	Thr	His	Asp	Pro	Asn	Val	Met	Arg
465					470						475				480
Pro	His	Ala	His	Asn	Asp	Phe	Tyr	Lys	Ala	His	Cys	Thr	Ser	His	Met
				485							490				495
Tyr	Glu	Leu	Ser	Leu	Ser	Ser	Phe	Ala	Ala	Trp	Trp	Thr	Met	Leu	Asn
			500							505					510
Ala	Leu	Ile	Leu	Met	Gly	Ala	Phe	Cys	Ile	Val	Leu	Arg	His	Cys	Cys
		515								520					525
Phe	Gln	Asn	Phe	Thr	Ala	Thr	Thr	Thr	Lys	Gly	Tyr	Tyr	Pro	Tyr	Asp
	530														540
Val	Pro	Asp	Tyr	Ala											
545															

<210> SEQ ID NO 66

<211> LENGTH: 3189

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Plasmid 3 insert - IgE leader + gH consensus + HA Tag + Furin + gL consensus +HA Tag nucleic acid sequence

<400> SEQUENCE: 66

```

atggactgga cctggatcct gttcctggtg gccgctgcta cccgggtgca cagtgcaccc    60
ggcctgcccc gctacctgac cgtgttcgcc gtgtacctgc tgagccatct gccagccag    120
agatacggcg ccgatgccgc ctctgaggcc ctggatcctc acgccttcca tctgtgtctg    180
aacacctacg gcagacctat ccggttctctg cgcgagaaca ccaccagtg cacctacaac    240
agcagcctgc ggaacagcac cgtcgtgcgc gagaatgcta tcagcttcaa cttcttcag    300
agctacaacc agtactacgt gttccacatg ccccggtgcc tgttcgccgg acctctggcc    360
gagcagttcc tgaaccaggt ggacctgacc gagacactgg aaagatacca gcagcggctg    420
aatacctacg ccctggtgtc caaggacctg gccagctacc ggctcttcag ccagcagctg    480
aaggctcagg acagcctggg cgagcagcct accaccgtgc cccctccaat cgacctgagc    540

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atcccccaag	tgtggatgcc	ccccagacc	acacctcacg	gctggaaaga	gagccacacc	600
accagcggcc	tgacacagacc	ccacttcaac	cagacctgca	ttctggtcga	cggccacgac	660
ctgctgttca	gcaccgtgac	cccctgctg	caccagggct	tctacctgat	cgacgagctg	720
agatacgtga	agatcacocct	gaccgaggat	ttcttctgtg	tcacctgtgc	catcgacgac	780
gacaccccc	tgctgctgat	cttcggccat	ctgcctcggg	tgctgttcaa	ggccccctac	840
cagcgggaca	acttcatoct	gcggcagacc	gagaagcacg	agctgctggg	gctggtaag	900
aaggaccagc	tgaaccggca	ctcctaactg	aaggaccccg	acttctctga	cgccgccttg	960
gacttcaact	acctggacct	gagcgccttg	ctgagaaaca	gcttccacag	atccgccttg	1020
gacgtgctga	agtcggcgcg	gtgccagatg	ctggacagac	ggacctgga	aatggccttc	1080
gcctatgccc	tggccctggt	tgccgcctct	cggcaggaag	aggctggcgc	tgaagtgtcc	1140
gtgccagag	ccctggacag	acaggccgct	ctgctgcaga	tccaggaatt	catgatcacc	1200
tgtctgagcc	agaccccccc	tggaccacc	ctgctgctgt	acctaccgc	cgtggatctg	1260
gccaagcggg	ccctgtggac	cccccaaccag	atcaccgaca	tcacaagcct	cgtgcggctg	1320
gtgtacatcc	tgagcaagca	gaaccagcag	cacctgatcc	cccagtgggc	cctgagacag	1380
atcgccgact	tcgccctgaa	gctgcacaag	accacactgg	ctagctttct	gagcgccttc	1440
gctaggcagg	aactgtacct	gatgggcagc	ctggtgcact	ccatgctggg	gcacaccacc	1500
gagagggcgg	aaatcttcat	cgtggaacc	ggcctgtgca	gcctggccga	gctgagccac	1560
ttcaccagc	tgctggccca	ccccaccac	gagtaactga	gcgacctgta	cacccccctg	1620
agctctagcg	gcagacggga	tcacagcctg	gaacggctga	cccggctggt	cccgatgcc	1680
acagtgcctg	ccactgtgcc	agccgccttg	tccatcctgt	ccaccatgca	gcccagcacc	1740
ctggaacct	tccccgaact	ggtctgctg	cccctggcgg	agagcttcag	cgccctgaca	1800
gtgtccgagc	acgtgtccta	cgtggtcacc	aaccagtacc	tgatcaaggg	catcagctac	1860
cccgtgtcca	ccaccgtcgt	gggccagagc	ctgatcatca	cccagaccga	cagccagacc	1920
aagtgcgagc	tgacccggaa	catgcacacc	acacacagca	tcaactgccgc	cctgaacatc	1980
agcctgga	actgcccctt	ctgccagtct	gccctgctgg	aatacgacga	taccagggc	2040
gtgatcaaca	tcatgtacat	gcacgacagc	gacgacgtgc	tgttgcacct	ggacccccctac	2100
aacgaggtgg	tggtgtccag	ccccgggacc	cactacctga	tgctgctgaa	gaacggcacc	2160
gtgctggaag	tgaccgacgt	ggtggtggac	gccaccgaca	gcagactgct	gatgatgagc	2220
gtgtacgccc	tgagcgcctc	catcggcctc	tacctgctgt	accggatgct	gaaaacctgc	2280
taccocctag	acgtgcccga	ctacgcccgc	ggcagaaaagc	ggagatcctg	cagggcggccc	2340
gactgcggct	tcagcttcag	ccctggcccc	gtgatcctgc	tgtggtgctg	cctgctgctg	2400
cccatcgtgt	cctctgcccgc	cgtgtctgtg	gccctacag	ccgccgagaa	ggtgccagcc	2460
gagtgccctg	agctgaccag	acgggtgtctg	ctgggcgagg	tgttccaggg	cgataagtac	2520
gagagctggc	tgcggccctt	ggtcaactgt	accggcagag	atggccccct	gagccagctg	2580
atccggta	gacccgtgac	ccctgaggcc	gccaacagcg	tgctgctgga	cgaagccttt	2640
ctggacacac	tggccctgct	gtacaacaac	cccgaccagc	tgccggccct	gctgacactg	2700
ctgagcagcg	ataccgcccc	cagatggatg	accgtgatgc	ggggctacag	cgagtgcggc	2760
gacggatctc	ccgccgtgta	cacctgtgtg	gacgacctgt	gccggggcta	cgacctgacc	2820
agactgagct	acggccggtc	catcttcaca	gagcacgtgc	tgggcttcga	gctggtgccc	2880
cccagcctgt	tcaatgtggg	ggtggccatc	cggaaacgag	ccaccggac	caacagagca	2940

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gtgcggtgc ctgtgtccac cgctgctgct ccagagggca tcacctgtt ctacggcctg 3000
tacaacgcgc tgaagagatt ctgcctgaga caccagctgg accccccct gctgcggcac 3060
ctggacaagt actacgcggc cctgcctccc gagctgaagc agaccagagt gaacctgccc 3120
gcccacagca gatacggccc tcaggcctg gagccagat acccttacga tgtgcctgat 3180
tatgcctga 3189

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<210> SEQ ID NO 67

<211> LENGTH: 1062

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

```

<223> OTHER INFORMATION: Plasmid 3 amino acid sequence - IgE leader + gH
consensus + HA Tag + Furin + gL consensus + HA Tag amino acid
sequence

```

<400> SEQUENCE: 67

```

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
1           5           10          15
His Ser Arg Pro Gly Leu Pro Ser Tyr Leu Thr Val Phe Ala Val Tyr
20          25          30
Leu Leu Ser His Leu Pro Ser Gln Arg Tyr Gly Ala Asp Ala Ala Ser
35          40          45
Glu Ala Leu Asp Pro His Ala Phe His Leu Leu Leu Asn Thr Tyr Gly
50          55          60
Arg Pro Ile Arg Phe Leu Arg Glu Asn Thr Thr Gln Cys Thr Tyr Asn
65          70          75          80
Ser Ser Leu Arg Asn Ser Thr Val Val Arg Glu Asn Ala Ile Ser Phe
85          90          95
Asn Phe Phe Gln Ser Tyr Asn Gln Tyr Tyr Val Phe His Met Pro Arg
100         105         110
Cys Leu Phe Ala Gly Pro Leu Ala Glu Gln Phe Leu Asn Gln Val Asp
115         120         125
Leu Thr Glu Thr Leu Glu Arg Tyr Gln Gln Arg Leu Asn Thr Tyr Ala
130         135         140
Leu Val Ser Lys Asp Leu Ala Ser Tyr Arg Ser Phe Ser Gln Gln Leu
145         150         155         160
Lys Ala Gln Asp Ser Leu Gly Glu Gln Pro Thr Thr Val Pro Pro Pro
165         170         175
Ile Asp Leu Ser Ile Pro His Val Trp Met Pro Pro Gln Thr Thr Pro
180         185         190
His Gly Trp Lys Glu Ser His Thr Thr Ser Gly Leu His Arg Pro His
195         200         205
Phe Asn Gln Thr Cys Ile Leu Phe Asp Gly His Asp Leu Leu Phe Ser
210         215         220
Thr Val Thr Pro Cys Leu His Gln Gly Phe Tyr Leu Ile Asp Glu Leu
225         230         235         240
Arg Tyr Val Lys Ile Thr Leu Thr Glu Asp Phe Phe Val Val Thr Val
245         250         255
Ser Ile Asp Asp Asp Thr Pro Met Leu Leu Ile Phe Gly His Leu Pro
260         265         270
Arg Val Leu Phe Lys Ala Pro Tyr Gln Arg Asp Asn Phe Ile Leu Arg
275         280         285
Gln Thr Glu Lys His Glu Leu Leu Val Leu Val Lys Lys Asp Gln Leu
290         295         300

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Asn Arg His Ser Tyr Leu Lys Asp Pro Asp Phe Leu Asp Ala Ala Leu
 305 310 315 320
 Asp Phe Asn Tyr Leu Asp Leu Ser Ala Leu Leu Arg Asn Ser Phe His
 325 330 335
 Arg Tyr Ala Val Asp Val Leu Lys Ser Gly Arg Cys Gln Met Leu Asp
 340 345 350
 Arg Arg Thr Val Glu Met Ala Phe Ala Tyr Ala Leu Ala Leu Phe Ala
 355 360 365
 Ala Ala Arg Gln Glu Glu Ala Gly Ala Glu Val Ser Val Pro Arg Ala
 370 375 380
 Leu Asp Arg Gln Ala Ala Leu Leu Gln Ile Gln Glu Phe Met Ile Thr
 385 390 395 400
 Cys Leu Ser Gln Thr Pro Pro Arg Thr Thr Leu Leu Leu Tyr Pro Thr
 405 410 415
 Ala Val Asp Leu Ala Lys Arg Ala Leu Trp Thr Pro Asn Gln Ile Thr
 420 425 430
 Asp Ile Thr Ser Leu Val Arg Leu Val Tyr Ile Leu Ser Lys Gln Asn
 435 440 445
 Gln Gln His Leu Ile Pro Gln Trp Ala Leu Arg Gln Ile Ala Asp Phe
 450 455 460
 Ala Leu Lys Leu His Lys Thr His Leu Ala Ser Phe Leu Ser Ala Phe
 465 470 475 480
 Ala Arg Gln Glu Leu Tyr Leu Met Gly Ser Leu Val His Ser Met Leu
 485 490 495
 Val His Thr Thr Glu Arg Arg Glu Ile Phe Ile Val Glu Thr Gly Leu
 500 505 510
 Cys Ser Leu Ala Glu Leu Ser His Phe Thr Gln Leu Leu Ala His Pro
 515 520 525
 His His Glu Tyr Leu Ser Asp Leu Tyr Thr Pro Cys Ser Ser Ser Gly
 530 535 540
 Arg Arg Asp His Ser Leu Glu Arg Leu Thr Arg Leu Phe Pro Asp Ala
 545 550 555 560
 Thr Val Pro Ala Thr Val Pro Ala Ala Leu Ser Ile Leu Ser Thr Met
 565 570 575
 Gln Pro Ser Thr Leu Glu Thr Phe Pro Asp Leu Phe Cys Leu Pro Leu
 580 585 590
 Gly Glu Ser Phe Ser Ala Leu Thr Val Ser Glu His Val Ser Tyr Val
 595 600 605
 Val Thr Asn Gln Tyr Leu Ile Lys Gly Ile Ser Tyr Pro Val Ser Thr
 610 615 620
 Thr Val Val Gly Gln Ser Leu Ile Ile Thr Gln Thr Asp Ser Gln Thr
 625 630 635 640
 Lys Cys Glu Leu Thr Arg Asn Met His Thr Thr His Ser Ile Thr Ala
 645 650 655
 Ala Leu Asn Ile Ser Leu Glu Asn Cys Ala Phe Cys Gln Ser Ala Leu
 660 665 670
 Leu Glu Tyr Asp Asp Thr Gln Gly Val Ile Asn Ile Met Tyr Met His
 675 680 685
 Asp Ser Asp Asp Val Leu Phe Ala Leu Asp Pro Tyr Asn Glu Val Val
 690 695 700
 Val Ser Ser Pro Arg Thr His Tyr Leu Met Leu Leu Lys Asn Gly Thr
 705 710 715 720

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tgcagagtgt ggctgagcgt gtgcctgtgc gccgtggtgc tgggccagtg ccagagagag 120
acagccgaga agaacgacta ctaccgggtg ccccaactact gggacgcctg ctctagagcc 180
ctgcccgaacc agacccggta caaatacgtg gaacagctgg tggacctgac cctgaactac 240
cactacgacg ccagccacgg cctggacaac ttcgacgtgc tgaagcggat caacgtgacc 300
gaggtgtccc tgctgatcag cgacttccgg cggcagaaca gaagaggcgg caccaacaag 360
cggactacct tcaacgcgcg tggcagcctg gccctcaacg ccagatccct ggaattcagc 420
gtgcggctgt tcgccaacta tccgtacgac gtcccagact acgccagagg ccggaagcgg 480
agatctctgc ggctgctgct gcggcaaccac ttccaactgcc tgctgctgtg tgccgtgtgg 540
gccacccctt gtctggccag cccttggagc accctgaccg ccaaccagaa ccctagcccc 600
ccctgggtcca agctgaccta cagcaagccc cagcagcgcg ctaccttcta ctgccattc 660
ctgtacccca gccctcccag aagcccctg cagttcagcg gcttccagcg ggtgtccacc 720
ggccctgagt gccggaacga gacactgtac ctgctgtaca accgcgaggg ccagaccctg 780
gtggaacggg ctagcacctg ggtcaagaaa gtgatctggt atctgagcgg ccggaaccag 840
accatcctgc agcggatgcc tcggaccgcc agcaagccta gcgacggcaa cgtgcagatc 900
agcgtggaag atgccaaaat cttcgcgccc cacatgggtgc ccaagcagac caagctgctg 960
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gcccacgtgt tccgggacta cagcgtgtca ttccaggtcc gactgacctt caccgaggcc 1080
aacaaccaga cctacacctt ctgcacccac cccaacctga tcgtctaccc ttacgacgtg 1140
ccagattatg ccaggggacg aaaaaggagg agcagcccca aggatctgac ccctttcctg 1200
accgcccctg ggctgctcct gggccacagc agagtgccta gagtgcgggc cgaggaatgc 1260
tgcgagttea tcaacgtgaa ccaccccccc gagcgggtgct acgacttcaa gatgtgcaac 1320
cggttcacgg tggtctgag atgccccgac ggccaagtgt gctacagccc cgagaaaacc 1380
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tgccgcaaag tgaacgacaa ggcccagtac ctgctgggcy ctgcaggcag tgtgccctac 1560
agatggatca acctggaata cgacaagatc acccggatcg tggcctgga ccagtacctg 1620
gaaagcgtga agaagcacia gcggctggac gtgtgccggg ccaagatggg ctacatgctg 1680
cagtaccat atgacgtccc cgattacgct tga 1713

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<210> SEQ ID NO 69

<211> LENGTH: 570

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

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<223> OTHER INFORMATION: Plasmid 5 amino acid sequence - IgE leader +
      UL131a consensus + HA Tag + Furin + UL130 consensus + HA Tag +
      Furin + UL128 consensus + HA Tag

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<400> SEQUENCE: 69

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Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
 1             5             10             15

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His Ser Arg Leu Cys Arg Val Trp Leu Ser Val Cys Leu Cys Ala Val
 20             25             30

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Val Leu Gly Gln Cys Gln Arg Glu Thr Ala Glu Lys Asn Asp Tyr Tyr
 35             40             45

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Arg Val Pro His Tyr Trp Asp Ala Cys Ser Arg Ala Leu Pro Asp Gln

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 atgctgaacg ccctgatoct gatggggcgc tctgcatcg tgetgcgga ctgctgcttc 1560

cagaacttca cgcaccacaac caccaagggc tactga 1596

<210> SEQ ID NO 71

<211> LENGTH: 531

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

 <223> OTHER INFORMATION: Plasmid 2 amino acid sequence version 2 - IgE
 leader + gM consensus + Furin + gN consensus amino acid sequence

<400> SEQUENCE: 71

 Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
 1 5 10 15

 His Ser Ala Pro Ser His Val Asp Lys Val Asn Thr Arg Thr Trp Ser
 20 25 30

 Ala Ser Ile Val Phe Met Val Leu Thr Phe Val Asn Val Ser Val His
 35 40 45

 Leu Val Leu Ser Asn Phe Pro His Leu Gly Tyr Pro Cys Val Tyr Tyr
 50 55 60

 His Val Val Asp Phe Glu Arg Leu Asn Met Ser Ala Tyr Asn Val Met
 65 70 75 80

 His Leu His Thr Pro Met Leu Phe Leu Asp Ser Val Gln Leu Val Cys
 85 90 95

 Tyr Ala Val Phe Met Gln Leu Val Phe Leu Ala Val Thr Ile Tyr Tyr
 100 105 110

 Leu Val Cys Trp Ile Lys Ile Ser Met Arg Lys Asp Lys Gly Met Ser
 115 120 125

 Leu Asn Gln Ser Thr Arg Asp Ile Ser Tyr Met Gly Asp Ser Leu Thr
 130 135 140

 Ala Phe Leu Phe Ile Leu Ser Met Asp Thr Phe Gln Leu Phe Thr Leu
 145 150 155 160

 Thr Met Ser Phe Arg Leu Pro Ser Met Ile Ala Phe Met Ala Ala Val
 165 170 175

 His Phe Phe Cys Leu Thr Ile Phe Asn Val Ser Met Val Thr Gln Tyr
 180 185 190

 Arg Ser Tyr Lys Arg Ser Leu Phe Phe Phe Ser Arg Leu His Pro Lys
 195 200 205

 Leu Lys Gly Thr Val Gln Phe Arg Thr Leu Ile Val Asn Leu Val Glu
 210 215 220

 Val Ala Leu Gly Phe Asn Thr Thr Val Val Ala Met Ala Leu Cys Tyr
 225 230 235 240

 Gly Phe Gly Asn Asn Phe Phe Val Arg Thr Gly His Met Val Leu Ala
 245 250 255

 Val Phe Val Val Tyr Ala Ile Ile Ser Ile Ile Tyr Phe Leu Leu Ile
 260 265 270

 Glu Ala Val Phe Phe Gln Tyr Val Lys Val Gln Phe Gly Tyr His Leu
 275 280 285

 Gly Ala Phe Phe Gly Leu Cys Gly Leu Ile Tyr Pro Ile Val Gln Tyr
 290 295 300

 Asp Thr Phe Leu Ser Asn Glu Tyr Arg Thr Gly Ile Ser Trp Ser Phe
 305 310 315 320

 Gly Met Leu Phe Phe Ile Trp Ala Met Phe Thr Thr Cys Arg Ala Val
 325 330 335

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Arg Tyr Phe Arg Gly Arg Gly Ser Gly Ser Val Lys Tyr Gln Ala Leu
 340 345 350

Ala Thr Ala Ser Gly Glu Glu Val Ala Ala Leu Ser His His Asp Ser
 355 360 365

Leu Glu Ser Arg Arg Leu Arg Glu Glu Glu Asp Asp Asp Asp Asp Glu
 370 375 380

Asp Phe Glu Asp Ala Arg Gly Arg Lys Arg Arg Ser Glu Trp Asn Thr
 385 390 395 400

Leu Val Leu Gly Leu Leu Val Leu Ser Val Ala Ala Ser Ser Asn Asn
 405 410 415

Thr Ser Thr Ala Ser Thr Pro Ser Pro Ser Ser Ser Thr His Thr Ser
 420 425 430

Thr Thr Val Lys Ala Thr Thr Thr Ala Thr Thr Ser Thr Thr Thr Ala
 435 440 445

Thr Ser Thr Thr Ser Ser Thr Thr Ser Thr Lys Pro Gly Ser Thr Thr
 450 455 460

His Asp Pro Asn Val Met Arg Pro His Ala His Asn Asp Phe Tyr Lys
 465 470 475 480

Ala His Cys Thr Ser His Met Tyr Glu Leu Ser Leu Ser Ser Phe Ala
 485 490 495

Ala Trp Trp Thr Met Leu Asn Ala Leu Ile Leu Met Gly Ala Phe Cys
 500 505 510

Ile Val Leu Arg His Cys Cys Phe Gln Asn Phe Thr Ala Thr Thr Thr
 515 520 525

Lys Gly Tyr
 530

<210> SEQ ID NO 72
 <211> LENGTH: 3135
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Plasmid 3 insert version 2 - IgE leader + gH
 consensus + Furin + gL consensus nucleic acid sequence

<400> SEQUENCE: 72

```

atggactgga cctggatcct gttcctgggtg gccgctgcta cccgggtgca cagtgcaccc    60
ggcctgcccc gctacctgac cgtgttgccc gtgtacctgc tgagccatct gccagccag    120
agatacggcg ccgatgccgc ctctgaggcc ctggatcctc acgccttcca tctgctgctg    180
aacacctacg gcagacctat ccggttctctg cgcgagaaca ccaccagtg cacctacaac    240
agcagcctgc ggaacagcac cgtcgtgcgc gagaatgcta tcagcttcaa cttcttcag    300
agctacaacc agtactacgt gttccacatg ccccggtgcc tggtcgccgg acctctggcc    360
gagcagttcc tgaaccaggt ggacctgacc gagacactgg aaagatacca gcagcggctg    420
aatacctaag ccctgggtgc caaggacctg gccagctacc ggtccttcag ccagcagctg    480
aaggctcagg acagcctggg cgagcagcct accaccgtgc cccctccaat cgacctgagc    540
atcccccaag tgtggatgcc cccccagacc acacctcagc gctggaaaga gagccacacc    600
accagcggcc tgcacagacc ccacttcaac cagacctgca ttctgttcga cggccacgac    660
ctgctgttca gcacctgac ccctgcctg caccagggct tctacctgat cgacgagctg    720
agatacgtga agatcacct gaccgaggat ttcttctgtg tcacctgtgc catcgacgac    780
gacacccccca tgetgctgat cttcgccat ctgcctcggg tgetgttcaa ggccccctac    840
cagcgggaca acttcactct gcggcagacc gagaagcacg agctgctggt gctggtcaag    900
    
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aaggaccagc tgaaccggca ctctactctg aaggaccccg acttctctgga cgcgcacctg	960
gacttcaact acctggacct gagcgacctg ctgagaaaca gcttccacag atacgacctg	1020
gacgtgctga agtccggccg gtgccagatg ctggacagac ggacctgga aatggacctc	1080
gcctatgcc tggccctggt tgcgcacctg cggcaggaag aggtggcgc tgaagtgtcc	1140
gtgccagag ccctggacag acaggccctg ctgctgcaga tccaggaatt catgatcacc	1200
tgtctgagcc agaccccc tccgaccacc ctgctgctgt accctaccgc cgtggatctg	1260
gccaagcggg ccctgtggac ccccaaccag atcaccgaca tcacaagcct cgtgcggctg	1320
gtgtacatcc tgagcaagca gaaccagcag cacctgatcc cccagtgggc cctgagacag	1380
atcggcact tccgctgaa gctgcacaag acccactctg ctagtcttct gagcgacctc	1440
gctaggcagg aactgtacct gatgggcagc ctggctgact ccatgctggt gcacaccacc	1500
gagagcggg aaatcttcat cgtggaaacc ggctgtgca gcctggccga gctgagccac	1560
ttcaccagc tctggccca cccccaccag gactacctga gcgacctgta cccccctgc	1620
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acagtgcctg cactgtgccc agccgacctg tccatcctgt ccaccatgca gccagcacc	1740
ctgaaacct tccccacct gttctgacct cccctggcgc agagcttcag cgcctgaca	1800
gtgtccgagc acgtgtccta cgtggtcacc aaccagtacc tgatcaaggc catcagctac	1860
cccgtgtcca ccaccgtctg gggccagagc ctgatcatca cccagaccga cagccagacc	1920
aagtgcgagc tgaccggaa catgcacacc acacacagca tcaactgccg cctgaacatc	1980
agcctgaaa actgcgacct ctgccagctt gccctgctgg aatacagcga taccagggc	2040
gtgatcaaca tcattgacat gcacgacagc gacgacgtgc tggctgacct ggaccctac	2100
aacgaggtgg tgggtgccc cccccggacc cactacctga tgctgctgaa gaacggcacc	2160
gtgctggaag tgaccgagc ggtggggac gccaccgaca gcagactgct gatgatgagc	2220
gtgtacgccc tgagcgccat catcgccatc tacctgctgt accggatgct gaaaacctgc	2280
cgcggcagaa agcggagatc ctgcagggcg cccgactgcg gcttcagctt cagccctggc	2340
cccgtgatcc tgetgtggtg ctgctgctg ctgcccctcg tgtcctctgc cgcctgtctt	2400
gtggccccta cagccgcca gaaggtgcca gccagtgcc ctgagctgac cagacgggtg	2460
ctgctggcgc aggtgttcca gggcgataag tacgagagct ggctgcggcc cctggtaaac	2520
gtgaccggca gagatggccc cctgagccag ctgatccggt acagaccctg gaccctgag	2580
gccccaaca gcgtgctgct ggacgaagcc tttctggaca cactggacct gctgtacaac	2640
aaccccgacc agctgcgggc cctgctgaca ctgctgagca gcgataccgc ccccagatgg	2700
atgaccgtga tgcggggcta cagcgagtgc ggcgacggat ctcccggct gtacacctgt	2760
gtggacgacc tgtgccgggg ctacgacctg accagactga gctacggccc gtccatcttc	2820
acagagcagc tgetgggctt cgagctggtg cccccagcc tggtaaatgt ggtggggccc	2880
atccggaacg aggccaccgc gaccaacaga gcagtgcggc tgcctgtgct caccgctgct	2940
gctccagagg gcataccct gttctacggc ctgtacaacg ccgtgaaaga gttctgctg	3000
agacaccagc tggaccccc cctgctgccc cacctggaca agtactaccg cggcctgctt	3060
cccagctga agcagaccag agtgaacctg cccgcccaca gcagatacgg ccctcaggcc	3120
gtggacgcca gatga	3135

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<211> LENGTH: 1044
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Plasmid 3 amino acid sequence version 2 - IgE
 leader + gH consensus + Furin + gL consensus nucleic acid sequence

<400> SEQUENCE: 73

Met Asp Trp Thr Trp Ile Leu Phe Leu Val Ala Ala Ala Thr Arg Val
 1 5 10 15
 His Ser Arg Pro Gly Leu Pro Ser Tyr Leu Thr Val Phe Ala Val Tyr
 20 25 30
 Leu Leu Ser His Leu Pro Ser Gln Arg Tyr Gly Ala Asp Ala Ala Ser
 35 40 45
 Glu Ala Leu Asp Pro His Ala Phe His Leu Leu Leu Asn Thr Tyr Gly
 50 55 60
 Arg Pro Ile Arg Phe Leu Arg Glu Asn Thr Thr Gln Cys Thr Tyr Asn
 65 70 75 80
 Ser Ser Leu Arg Asn Ser Thr Val Val Arg Glu Asn Ala Ile Ser Phe
 85 90 95
 Asn Phe Phe Gln Ser Tyr Asn Gln Tyr Tyr Val Phe His Met Pro Arg
 100 105 110
 Cys Leu Phe Ala Gly Pro Leu Ala Glu Gln Phe Leu Asn Gln Val Asp
 115 120 125
 Leu Thr Glu Thr Leu Glu Arg Tyr Gln Gln Arg Leu Asn Thr Tyr Ala
 130 135 140
 Leu Val Ser Lys Asp Leu Ala Ser Tyr Arg Ser Phe Ser Gln Gln Leu
 145 150 155 160
 Lys Ala Gln Asp Ser Leu Gly Glu Gln Pro Thr Thr Val Pro Pro Pro
 165 170 175
 Ile Asp Leu Ser Ile Pro His Val Trp Met Pro Pro Gln Thr Thr Pro
 180 185 190
 His Gly Trp Lys Glu Ser His Thr Thr Ser Gly Leu His Arg Pro His
 195 200 205
 Phe Asn Gln Thr Cys Ile Leu Phe Asp Gly His Asp Leu Leu Phe Ser
 210 215 220
 Thr Val Thr Pro Cys Leu His Gln Gly Phe Tyr Leu Ile Asp Glu Leu
 225 230 235 240
 Arg Tyr Val Lys Ile Thr Leu Thr Glu Asp Phe Phe Val Val Thr Val
 245 250 255
 Ser Ile Asp Asp Asp Thr Pro Met Leu Leu Ile Phe Gly His Leu Pro
 260 265 270
 Arg Val Leu Phe Lys Ala Pro Tyr Gln Arg Asp Asn Phe Ile Leu Arg
 275 280 285
 Gln Thr Glu Lys His Glu Leu Leu Val Leu Val Lys Lys Asp Gln Leu
 290 295 300
 Asn Arg His Ser Tyr Leu Lys Asp Pro Asp Phe Leu Asp Ala Ala Leu
 305 310 315 320
 Asp Phe Asn Tyr Leu Asp Leu Ser Ala Leu Leu Arg Asn Ser Phe His
 325 330 335
 Arg Tyr Ala Val Asp Val Leu Lys Ser Gly Arg Cys Gln Met Leu Asp
 340 345 350
 Arg Arg Thr Val Glu Met Ala Phe Ala Tyr Ala Leu Ala Leu Phe Ala
 355 360 365
 Ala Ala Arg Gln Glu Glu Ala Gly Ala Glu Val Ser Val Pro Arg Ala

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370					375					380					
Leu	Asp	Arg	Gln	Ala	Ala	Leu	Leu	Gln	Ile	Gln	Glu	Phe	Met	Ile	Thr
385					390					395					400
Cys	Leu	Ser	Gln	Thr	Pro	Pro	Arg	Thr	Thr	Leu	Leu	Leu	Tyr	Pro	Thr
				405					410					415	
Ala	Val	Asp	Leu	Ala	Lys	Arg	Ala	Leu	Trp	Thr	Pro	Asn	Gln	Ile	Thr
				420					425					430	
Asp	Ile	Thr	Ser	Leu	Val	Arg	Leu	Val	Tyr	Ile	Leu	Ser	Lys	Gln	Asn
				435					440					445	
Gln	Gln	His	Leu	Ile	Pro	Gln	Trp	Ala	Leu	Arg	Gln	Ile	Ala	Asp	Phe
				450					455					460	
Ala	Leu	Lys	Leu	His	Lys	Thr	His	Leu	Ala	Ser	Phe	Leu	Ser	Ala	Phe
				465					470					475	
Ala	Arg	Gln	Glu	Leu	Tyr	Leu	Met	Gly	Ser	Leu	Val	His	Ser	Met	Leu
				485					490					495	
Val	His	Thr	Thr	Glu	Arg	Arg	Glu	Ile	Phe	Ile	Val	Glu	Thr	Gly	Leu
				500					505					510	
Cys	Ser	Leu	Ala	Glu	Leu	Ser	His	Phe	Thr	Gln	Leu	Leu	Ala	His	Pro
				515					520					525	
His	His	Glu	Tyr	Leu	Ser	Asp	Leu	Tyr	Thr	Pro	Cys	Ser	Ser	Ser	Gly
				530					535					540	
Arg	Arg	Asp	His	Ser	Leu	Glu	Arg	Leu	Thr	Arg	Leu	Phe	Pro	Asp	Ala
				545					550					555	
Thr	Val	Pro	Ala	Thr	Val	Pro	Ala	Ala	Leu	Ser	Ile	Leu	Ser	Thr	Met
				565					570					575	
Gln	Pro	Ser	Thr	Leu	Glu	Thr	Phe	Pro	Asp	Leu	Phe	Cys	Leu	Pro	Leu
				580					585					590	
Gly	Glu	Ser	Phe	Ser	Ala	Leu	Thr	Val	Ser	Glu	His	Val	Ser	Tyr	Val
				595					600					605	
Val	Thr	Asn	Gln	Tyr	Leu	Ile	Lys	Gly	Ile	Ser	Tyr	Pro	Val	Ser	Thr
				610					615					620	
Thr	Val	Val	Gly	Gln	Ser	Leu	Ile	Ile	Thr	Gln	Thr	Asp	Ser	Gln	Thr
				625					630					635	
Lys	Cys	Glu	Leu	Thr	Arg	Asn	Met	His	Thr	Thr	His	Ser	Ile	Thr	Ala
				645					650					655	
Ala	Leu	Asn	Ile	Ser	Leu	Glu	Asn	Cys	Ala	Phe	Cys	Gln	Ser	Ala	Leu
				660					665					670	
Leu	Glu	Tyr	Asp	Asp	Thr	Gln	Gly	Val	Ile	Asn	Ile	Met	Tyr	Met	His
				675					680					685	
Asp	Ser	Asp	Asp	Val	Leu	Phe	Ala	Leu	Asp	Pro	Tyr	Asn	Glu	Val	Val
				690					695					700	
Val	Ser	Ser	Pro	Arg	Thr	His	Tyr	Leu	Met	Leu	Leu	Lys	Asn	Gly	Thr
				705					710					715	
Val	Leu	Glu	Val	Thr	Asp	Val	Val	Val	Asp	Ala	Thr	Asp	Ser	Arg	Leu
				725					730					735	
Leu	Met	Met	Ser	Val	Tyr	Ala	Leu	Ser	Ala	Ile	Ile	Gly	Ile	Tyr	Leu
				740					745					750	
Leu	Tyr	Arg	Met	Leu	Lys	Thr	Cys	Arg	Gly	Arg	Lys	Arg	Arg	Ser	Cys
				755					760					765	
Arg	Arg	Pro	Asp	Cys	Gly	Phe	Ser	Phe	Ser	Pro	Gly	Pro	Val	Ile	Leu
				770					775					780	
Leu	Trp	Cys	Cys	Leu	Leu	Leu	Pro	Ile	Val	Ser	Ser	Ala	Ala	Val	Ser
				785					790					795	
															800

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agcaccctga cgcacca caaaccctagc cccccctggt ccaagctgac ctacagcaag 600
ccccacgacg ccgctacctt ctactgocca ttctgtacc ccagccctcc cagaagcccc 660
ctgcagttca gcggttoca gcggtgtcc accggccctg agtgccgga cgagacactg 720
tacctgctgt acaaccgoga gggccagacc ctggtggaac ggtctagcac ctgggtcaag 780
aaagtgatct ggtatctgag cggccggaac cagaccatcc tgcagcggat gcctcggacc 840
gccagcaagc ctagcgacg caactgtcag atcagcgtgg aagatgcca aatcttcggc 900
gcccacatgg tgcccaagca gaccaagctg ctgagattcg tggtaacga cggcaccaga 960
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gaatgctgag agttcatcaa cgtgaaccac ccccccgagc ggtgctacga cttcaagatg 1260
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<210> SEQ ID NO 75

<211> LENGTH: 543

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

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<223> OTHER INFORMATION: Plasmid 5 amino acid sequence version 2 - IgE
leader + UL131a consensus + Furin + UL130 consensus + Furin +
UL128 consensus amino acid sequence

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<400> SEQUENCE: 75

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20          25          30
Val Leu Gly Gln Cys Gln Arg Glu Thr Ala Glu Lys Asn Asp Tyr Tyr
35          40          45
Arg Val Pro His Tyr Trp Asp Ala Cys Ser Arg Ala Leu Pro Asp Gln
50          55          60
Thr Arg Tyr Lys Tyr Val Glu Gln Leu Val Asp Leu Thr Leu Asn Tyr
65          70          75          80
His Tyr Asp Ala Ser His Gly Leu Asp Asn Phe Asp Val Leu Lys Arg
85          90          95
Ile Asn Val Thr Glu Val Ser Leu Leu Ile Ser Asp Phe Arg Arg Gln
100         105         110
Asn Arg Arg Gly Gly Thr Asn Lys Arg Thr Thr Phe Asn Ala Ala Gly
115         120         125
Ser Leu Ala Pro His Ala Arg Ser Leu Glu Phe Ser Val Arg Leu Phe
130         135         140
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 <223> OTHER INFORMATION: modified pVax1 backbone nucleic acid sequence

<400> SEQUENCE: 76

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aatgacgtat gttcccatag taacgccaat agggactttc cattgacgtc aatgggtgga    240
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gcggttttgg cagtacatca atgggcgtgg atagcggttt gactcacggg gatttccaag    480
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<210> SEQ ID NO 77

<211> LENGTH: 5742

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: 1011932_pHCMVgB_pVAX1 (LTGA)

<400> SEQUENCE: 77

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<211> LENGTH: 4590

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: 1007652_pHCMVgMgN_pVAX1 (LTGA)

<400> SEQUENCE: 78

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<211> LENGTH: 6129

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

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<223> OTHER INFORMATION: 0958364_pCMVgHgL_pVAX1 (LTGA)

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<210> SEQ ID NO 80

<211> LENGTH: 4437

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

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<400> SEQUENCE: 80

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<210> SEQ ID NO 81

<211> LENGTH: 4653

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: 1007656_pHCMVgUL_pVAX1 (LTGA)

<400> SEQUENCE: 81

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<211> LENGTH: 5715

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: 1028044_pHCMV_gB_pVAX1 (LGA)

<400> SEQUENCE: 82

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<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

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<400> SEQUENCE: 83

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<210> SEQ ID NO 84
 <211> LENGTH: 4671
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: 103600_pHCMV_UL83_pVAX1 (LGS)

<400> SEQUENCE: 84

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<210> SEQ ID NO 85
<211> LENGTH: 904
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: pHSV1-gB Amino Acid Sequence

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<400> SEQUENCE: 85

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20          25          30
Ser Ser Pro Gly Thr Pro Gly Val Ala Ala Ala Thr Gln Ala Ala Asn
35          40          45
Gly Gly Pro Ala Thr Pro Ala Pro Pro Ala Pro Gly Pro Ala Pro Thr
50          55          60
Gly Asp Thr Lys Pro Lys Lys Asn Lys Lys Pro Lys Pro Pro Pro Pro
65          70          75          80
Pro Arg Pro Ala Gly Asp Asn Ala Thr Val Ala Ala Gly His Ala Thr
85          90          95
Leu Arg Glu His Leu Arg Asp Ile Lys Ala Glu Asn Thr Asp Ala Asn
100         105         110
Phe Tyr Val Cys Pro Pro Pro Thr Gly Ala Thr Val Val Gln Phe Glu
115         120         125
Gln Pro Arg Arg Cys Pro Thr Arg Pro Glu Gly Gln Asn Tyr Thr Glu
130         135         140
Gly Ile Ala Val Val Phe Lys Glu Asn Ile Ala Pro Tyr Lys Phe Lys
145         150         155         160
Ala Thr Met Tyr Tyr Lys Asp Val Thr Val Ser Gln Val Trp Phe Gly
165         170         175
His Arg Tyr Ser Gln Phe Met Gly Ile Phe Glu Asp Arg Ala Pro Val
180         185         190
Pro Phe Glu Glu Val Ile Asp Lys Ile Asn Ala Lys Gly Val Cys Arg
195         200         205
Ser Thr Ala Lys Tyr Val Arg Asn Asn Leu Glu Thr Thr Ala Phe His
210         215         220
Arg Asp Asp His Glu Thr Asp Met Glu Leu Lys Pro Ala Asn Ala Ala
225         230         235         240
Thr Arg Thr Ser Arg Gly Trp His Thr Thr Asp Leu Lys Tyr Asn Pro
245         250         255
Ser Arg Val Glu Ala Phe His Arg Tyr Gly Thr Thr Val Asn Cys Ile
260         265         270
Val Glu Glu Val Asp Ala Arg Ser Val Tyr Pro Tyr Asp Glu Phe Val
275         280         285
Leu Ala Thr Gly Asp Phe Val Tyr Met Ser Pro Phe Tyr Gly Tyr Arg
290         295         300
Glu Gly Ser His Thr Glu His Thr Ser Tyr Ala Ala Asp Arg Phe Lys
305         310         315         320

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Ala Phe Phe Glu Gly Met Gly Asp Leu Gly Arg Ala Val Gly Lys Val
740 745 750

Val Met Gly Ile Val Gly Gly Val Val Ser Ala Val Ser Gly Val Ser
755 760 765

Ser Phe Met Ser Asn Pro Phe Gly Ala Leu Ala Val Gly Leu Leu Val
770 775 780

Leu Ala Gly Leu Ala Ala Ala Phe Phe Ala Phe Arg Tyr Val Met Arg
785 790 795 800

Leu Gln Ser Asn Pro Met Lys Ala Leu Tyr Pro Leu Thr Thr Lys Glu
805 810 815

Leu Lys Asn Pro Thr Asn Pro Asp Ala Ser Gly Glu Gly Glu Glu Gly
820 825 830

Gly Asp Phe Asp Glu Ala Lys Leu Ala Glu Ala Arg Glu Met Ile Arg
835 840 845

Tyr Met Ala Leu Val Ser Ala Met Glu Arg Thr Glu His Lys Ala Lys
850 855 860

Lys Lys Gly Thr Ser Ala Leu Leu Ser Ala Lys Val Thr Asp Met Val
865 870 875 880

Met Arg Lys Arg Arg Asn Thr Asn Tyr Thr Gln Val Pro Asn Lys Asp
885 890 895

Gly Asp Ala Asp Glu Asp Asp Leu
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<210> SEQ ID NO 86

<211> LENGTH: 2715

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: pHSV1-gB nucleic acid sequence

<400> SEQUENCE: 86

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gcagcagcta cccaggcagc aaacggcgga ccagctacc ctgcaccccc tgcacctgga 180
ccagcaccaa ctggcgatac caaaccaaag aaaaacaaga aaccaaagcc accccctcca 240
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<210> SEQ ID NO 87

<211> LENGTH: 1068

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: pHSV1-gHgL amino acid sequence

<400> SEQUENCE: 87

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Met Gly Asn Gly Leu Trp Phe Val Gly Val Ile Ile Leu Gly Val Ala
 1             5             10             15

Trp Gly Gln Val His Asp Trp Thr Glu Gln Thr Asp Pro Trp Phe Leu
 20             25             30

Asp Gly Leu Gly Met Asp Arg Met Tyr Trp Arg Asp Thr Asn Thr Gly
 35             40             45

Arg Leu Trp Leu Pro Asn Thr Pro Asp Pro Gln Lys Pro Pro Arg Gly
 50             55             60

Phe Leu Ala Pro Pro Asp Glu Leu Asn Leu Thr Thr Ala Ser Leu Pro

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65	70	75	80
Leu Leu Arg Trp Tyr Glu Glu Arg Phe Cys Phe Val Leu Val Thr Thr 85 90 95			
Ala Glu Phe Pro Arg Asp Pro Gly Gln Leu Leu Tyr Ile Pro Lys Thr 100 105 110			
Tyr Leu Leu Gly Arg Pro Pro Asn Ala Ser Leu Pro Ala Pro Thr Thr 115 120 125			
Val Glu Pro Thr Ala Gln Pro Pro Pro Ser Val Ala Pro Leu Lys Gly 130 135 140			
Leu Leu His Asn Pro Ala Ala Ser Val Leu Leu Arg Ser Arg Ala Trp 145 150 155 160			
Val Thr Phe Ser Ala Val Pro Asp Pro Glu Ala Leu Thr Phe Pro Arg 165 170 175			
Gly Asp Asn Val Ala Thr Ala Ser His Pro Ser Gly Pro Arg Asp Thr 180 185 190			
Pro Pro Pro Arg Pro Pro Val Gly Ala Arg Arg His Pro Thr Thr Glu 195 200 205			
Leu Asp Ile Thr His Leu His Asn Ala Ser Thr Thr Trp Leu Ala Thr 210 215 220			
Arg Gly Leu Leu Arg Ser Pro Gly Arg Tyr Val Tyr Phe Ser Pro Ser 225 230 235 240			
Ala Ser Thr Trp Pro Val Gly Ile Trp Thr Thr Gly Glu Leu Val Leu 245 250 255			
Gly Cys Asp Ala Ala Leu Val Arg Ala Arg Tyr Gly Arg Glu Phe Met 260 265 270			
Gly Leu Val Ile Ser Met His Asp Ser Pro Pro Val Glu Val Met Val 275 280 285			
Val Pro Ala Gly Gln Thr Leu Asp Arg Val Gly Asp Pro Ala Asp Glu 290 295 300			
Asn Pro Pro Gly Ala Leu Pro Gly Pro Pro Gly Gly Pro Arg Tyr Arg 305 310 315 320			
Val Phe Val Leu Gly Ser Leu Thr Arg Ala Asp Asn Gly Ser Ala Leu 325 330 335			
Asp Ala Leu Arg Arg Val Gly Gly Tyr Pro Glu Glu Gly Thr Asn Tyr 340 345 350			
Ala Gln Phe Leu Ser Arg Ala Tyr Ala Glu Phe Phe Ser Gly Asp Ala 355 360 365			
Gly Ala Glu Gln Gly Pro Arg Pro Pro Leu Phe Trp Arg Leu Thr Gly 370 375 380			
Leu Leu Ala Thr Ser Gly Phe Ala Phe Val Asn Ala Ala His Ala Asn 385 390 395 400			
Gly Ala Val Cys Leu Ser Asp Leu Leu Gly Phe Leu Ala His Ser Arg 405 410 415			
Ala Leu Ala Gly Leu Ala Ala Arg Gly Ala Ala Gly Cys Ala Ala Asp 420 425 430			
Ser Val Phe Phe Asn Val Ser Val Leu Asp Pro Thr Ala Arg Leu Gln 435 440 445			
Leu Glu Ala Arg Leu Gln His Leu Val Ala Glu Ile Leu Glu Arg Glu 450 455 460			
Gln Ser Leu Ala Leu His Ala Leu Gly Tyr Gln Leu Ala Phe Val Leu 465 470 475 480			
Asp Ser Pro Ser Ala Tyr Asp Ala Val Ala Pro Ser Ala Ala His Leu 485 490 495			

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Gly Ile Phe Leu Arg Tyr His Cys Pro Gly Leu Asp Thr Val Leu Trp
915 920 925

Asp Arg His Ala Gln Lys Ala Tyr Trp Val Asn Pro Phe Leu Phe Val
930 935 940

Ala Gly Phe Leu Glu Asp Leu Ser His Pro Ala Phe Pro Ala Asn Thr
945 950 955 960

Gln Glu Thr Glu Thr Arg Leu Ala Leu Tyr Lys Glu Ile Arg Gln Ala
965 970 975

Leu Asp Ser Arg Lys Gln Ala Ala Ser His Thr Pro Val Lys Ala Gly
980 985 990

Cys Val Asn Phe Asp Tyr Ser Arg Thr Arg Arg Cys Val Gly Arg Gln
995 1000 1005

Asp Leu Gly Pro Thr Asn Gly Thr Ser Gly Arg Thr Pro Val Leu
1010 1015 1020

Pro Pro Asp Asp Glu Ala Gly Leu Gln Pro Lys Pro Leu Thr Thr
1025 1030 1035

Pro Pro Pro Ile Ile Ala Thr Ser Asp Pro Thr Pro Arg Arg Asp
1040 1045 1050

Ala Ala Thr Lys Ser Arg Arg Arg Arg Pro His Ser Arg Arg Leu
1055 1060 1065

<210> SEQ ID NO 88
<211> LENGTH: 3207
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: pHSV1-gHgL nucleic acid sequence

<400> SEQUENCE: 88

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atggggaaacg ggctgtggtt tgtcggagtg attatcctgg gcgtcgcgatg gggacagggtg    60
catgactgga ctgaacagac tgatccttgg ttcctggacg ggctgggaat ggatcgcgatg    120
tactggcgag acacaaacac tggcaggctg tggctgccaa ataccccaga tcctcagaag    180
ccccctcgcg ggtttctggc tccaccgac gagctgaacc tgaccacagc cagcctgcca    240
ctgctgcgat ggtatgagga acgattctgc tttgtgctgg tcaactaccg agaattcccc    300
egggaccctg gacagctgct gtacatccct aagacctatc tgctgggaag acctccaaac    360
gctagtctgc cagcaccac aactgtcgag ccaacagctc agccccctcc atccgtggca    420
ccactgaaag gcctgctgca caatccagca gcttccgtgc tgctgcgatc tcgggcctgg    480
gtcacattct ccgctgtgcc tgaccagag gcaactgacct tccccgggg agataacgtg    540
gcaacagcct ctcacccaag tggccccagg gacaccctc ctccccggcc tcccgtggga    600
gcacggagac atcccaccac agaactggat atcacacacc tgcataatgc cagcactacc    660
tggctgggta ctcggggct gctgagatcc cctgggaggt acgtgtatct ttctcccagt    720
gcctcaacat ggctgtggg aatctggaca actggcgagc tggctcctggg gtgtgatgca    780
gccctggtga gagccagata cggacgggag ttcatgggcc tggatcctc aatgcacgac    840
agcccaccog tggaaatcat ggtggtccct gccgggcaga ccctggatag agtgggagac    900
ccagccgatg aaaaccctcc aggggctctg ccaggacccc ctggcgggcc acgctaccga    960
gtgtttgtcc tgggcagcct gactagggcc gacaacgggt ccgctctgga tgcactgagg   1020
cgctggggag gctacctga ggaaggcacc aattatgccc agttcctgct tcgcttatt   1080
gcagagttct ttagtggaga cgcaggagct gaacagggac cagcaccacc cctgttttgg   1140
cggctgacog gactgctggc aacaagcgcc ttcgcctttg tcaacgctgc acagccaat   1200

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ggggccgtgt gcctgtccga tctgtggga ttctggcac attctagggc actggcagga 1260
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ctggatccca ccgcaagact gcagctggag gcaaggctgc agcacctggt ggccgaaatc 1380
ctggagaggg aacagagcct ggcactgcat gccctggggg accagctggc tttcgtcctg 1440
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gcacagcaga cacacggact ggcattccacc ctgacacgat gggccatta caatgtcctg 1920
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ccaaggatcc tgggtcccat tacacacaat gccagctacg tggtaactca tagcccctg 2040
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tacctgactg ccacctgtga gggatctacc agagatattg aaagtaaaag actggtgagg 2160
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gagaccctt cagccatcaa ttatgctctg atcgatggca ttttctgctg gtacctgctc 2760
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acccggcggg gcgtggggag acaggatctg ggaccaacta atggaaccag cggcagaact 3060
cccgtgctgc ctccagacga tgaggctgga ctgcagccta aacctgac taccctccc 3120
ccaatcattg ccaccagcga cccacacccc cgacgagatg ctgccaccaa gtcaagacgc 3180
cgacgcccc actcaagacg cctgtgta 3207

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<210> SEQ ID NO 89

<211> LENGTH: 911

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: pHSV1-gCgD amino acid sequence

<400> SEQUENCE: 89

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Met Ala Pro Gly Arg Val Gly Leu Ala Val Val Leu Trp Ser Leu Leu
 1 5 10 15
 Trp Leu Gly Ala Gly Val Ser Gly Gly Ser Glu Thr Ala Ser Thr Gly
 20 25 30
 Pro Thr Ile Thr Ala Gly Ala Val Thr Asn Ala Ser Glu Ala Pro Thr
 35 40 45
 Ser Gly Ser Pro Gly Ser Ala Ala Ser Pro Glu Val Thr Pro Thr Ser
 50 55 60
 Thr Pro Asn Pro Asn Asn Val Thr Gln Asn Lys Thr Thr Pro Thr Glu
 65 70 75 80
 Pro Ala Ser Pro Pro Thr Thr Pro Lys Pro Thr Ser Thr Pro Lys Ser
 85 90 95
 Pro Pro Thr Ser Thr Pro Asp Pro Lys Pro Lys Asn Asn Thr Thr Pro
 100 105 110
 Ala Lys Ser Gly Arg Pro Thr Lys Pro Pro Gly Pro Val Trp Cys Asp
 115 120 125
 Arg Arg Asp Pro Leu Ala Arg Tyr Gly Ser Arg Val Gln Ile Arg Cys
 130 135 140
 Arg Phe Arg Asn Ser Thr Arg Met Glu Phe Arg Leu Gln Ile Trp Arg
 145 150 155 160
 Tyr Ser Met Gly Pro Ser Pro Pro Ile Ala Pro Ala Pro Asp Leu Glu
 165 170 175
 Glu Val Leu Thr Asn Ile Thr Ala Pro Pro Gly Gly Leu Leu Val Tyr
 180 185 190
 Asp Ser Ala Pro Asn Leu Thr Asp Pro His Val Leu Trp Ala Glu Gly
 195 200 205
 Ala Gly Pro Gly Ala Asp Pro Pro Leu Tyr Ser Val Thr Gly Pro Leu
 210 215 220
 Pro Thr Gln Arg Leu Ile Ile Gly Glu Val Thr Pro Ala Thr Gln Gly
 225 230 235 240
 Met Tyr Tyr Leu Ala Trp Gly Arg Met Asp Ser Pro His Glu Tyr Gly
 245 250 255
 Thr Trp Val Arg Val Arg Met Phe Arg Pro Pro Ser Leu Thr Leu Gln
 260 265 270
 Pro His Ala Val Met Glu Gly Gln Pro Phe Lys Ala Thr Cys Thr Ala
 275 280 285
 Ala Ala Tyr Tyr Pro Arg Asn Pro Val Glu Phe Val Trp Phe Glu Asp
 290 295 300
 Asp Arg Gln Val Phe Asn Pro Gly Gln Ile Asp Thr Gln Thr His Glu
 305 310 315 320
 His Pro Asp Gly Phe Thr Thr Val Ser Thr Val Thr Ser Glu Ala Val
 325 330 335
 Gly Gly Gln Val Pro Pro Arg Thr Phe Thr Cys Gln Met Thr Trp His
 340 345 350
 Arg Asp Ser Val Thr Phe Ser Arg Arg Asn Ala Thr Gly Leu Ala Leu
 355 360 365
 Val Leu Pro Arg Pro Thr Ile Thr Met Glu Phe Gly Val Arg His Val
 370 375 380
 Val Cys Thr Ala Gly Cys Val Pro Glu Gly Val Thr Phe Ala Trp Phe
 385 390 395 400
 Leu Gly Asp Asp Pro Ser Pro Ala Ala Lys Ser Ala Val Thr Ala Gln
 405 410 415
 Glu Ser Cys Asp His Pro Gly Leu Ala Thr Val Arg Ser Thr Leu Pro

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420					425					430					
Ile	Ser	Tyr	Asp	Tyr	Ser	Glu	Tyr	Ile	Cys	Arg	Leu	Thr	Gly	Tyr	Pro
	435						440					445			
Ala	Gly	Ile	Pro	Val	Leu	Glu	His	His	Gly	Ser	His	Gln	Pro	Pro	Pro
	450					455					460				
Arg	Asp	Pro	Thr	Glu	Arg	Gln	Val	Ile	Glu	Ala	Ile	Glu	Trp	Val	Gly
	465					470					475				480
Ile	Gly	Ile	Gly	Val	Leu	Ala	Ala	Gly	Val	Leu	Val	Val	Thr	Ala	Ile
				485					490					495	
Val	Tyr	Val	Val	Arg	Thr	Ser	Gln	Ser	Arg	Gln	Arg	His	Arg	Arg	Arg
				500					505					510	
Gly	Arg	Lys	Arg	Arg	Ser	Gly	Gly	Ala	Ala	Ala	Arg	Leu	Gly	Ala	Val
		515					520					525			
Ile	Leu	Phe	Val	Val	Ile	Val	Gly	Leu	His	Gly	Val	Arg	Gly	Lys	Tyr
	530					535						540			
Ala	Leu	Ala	Asp	Ala	Ser	Leu	Lys	Met	Ala	Asp	Pro	Asn	Arg	Phe	Arg
	545					550					555				560
Gly	Lys	Asp	Leu	Pro	Val	Leu	Asp	Gln	Leu	Thr	Asp	Pro	Pro	Gly	Val
				565					570					575	
Arg	Arg	Val	Tyr	His	Ile	Gln	Ala	Gly	Leu	Pro	Asn	Pro	Phe	Gln	Pro
				580					585					590	
Pro	Ser	Leu	Pro	Ile	Thr	Val	Tyr	Tyr	Ala	Val	Leu	Glu	Arg	Ala	Cys
		595					600					605			
Arg	Ser	Val	Leu	Leu	Asn	Ala	Pro	Ser	Glu	Ala	Pro	Gln	Ile	Val	Arg
	610					615					620				
Gly	Ala	Ser	Glu	Asp	Val	Arg	Lys	Gln	Pro	Tyr	Asn	Leu	Thr	Ile	Ala
	625					630					635				640
Trp	Phe	Arg	Met	Gly	Gly	Asn	Cys	Ala	Ile	Pro	Ile	Thr	Val	Met	Glu
				645					650					655	
Tyr	Thr	Glu	Cys	Ser	Tyr	Asn	Lys	Ser	Leu	Gly	Ala	Cys	Pro	Ile	Arg
			660						665					670	
Thr	Gln	Pro	Arg	Trp	Asn	Tyr	Tyr	Asp	Ser	Phe	Ser	Ala	Val	Ser	Glu
		675					680						685		
Asp	Asn	Leu	Gly	Phe	Leu	Met	His	Ala	Pro	Ala	Phe	Glu	Thr	Ala	Gly
	690					695					700				
Thr	Tyr	Leu	Arg	Leu	Val	Lys	Ile	Asn	Asp	Trp	Thr	Glu	Ile	Thr	Gln
	705					710					715				720
Phe	Ile	Leu	Glu	His	Arg	Ala	Lys	Gly	Ser	Cys	Lys	Tyr	Ala	Leu	Pro
				725					730					735	
Leu	Arg	Ile	Pro	Pro	Ser	Ala	Cys	Leu	Ser	Pro	Gln	Ala	Tyr	Gln	Gln
			740						745					750	
Gly	Val	Thr	Val	Asp	Ser	Ile	Gly	Met	Leu	Pro	Arg	Phe	Ile	Pro	Glu
		755					760					765			
Asn	Gln	Arg	Thr	Val	Ala	Val	Tyr	Ser	Leu	Lys	Ile	Ala	Gly	Trp	His
	770					775					780				
Gly	Pro	Lys	Ala	Pro	Tyr	Thr	Ser	Thr	Leu	Leu	Pro	Pro	Glu	Leu	Ser
				785		790					795				800
Glu	Thr	Pro	Asn	Ala	Thr	Gln	Pro	Glu	Leu	Ala	Pro	Glu	Asp	Pro	Glu
				805					810					815	
Asp	Ser	Ala	Leu	Leu	Glu	Asp	Pro	Val	Gly	Thr	Val	Ala	Pro	Gln	Ile
			820						825					830	
Pro	Pro	Asn	Trp	His	Ile	Pro	Ser	Ile	Gln	Asp	Ala	Ala	Thr	Pro	Tyr
			835						840					845	

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His Pro Pro Ala Thr Pro Asn Asn Met Gly Leu Ile Ala Gly Ala Val
850 855 860

Gly Gly Ser Leu Leu Ala Ala Leu Val Ile Cys Gly Ile Val Tyr Trp
865 870 875 880

Met Arg Arg Arg Thr Arg Lys Ala Pro Lys Arg Ile Arg Leu Pro His
885 890 895

Ile Arg Glu Asp Asp Gln Pro Ser Ser His Gln Pro Leu Phe Tyr
900 905 910

<210> SEQ ID NO 90
<211> LENGTH: 2736
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: pHSV1-gCgD nucleic acid sequence

<400> SEQUENCE: 90

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ggcgtgagcg gcgatcaga aactgcaagt accggaceta ctatcacgcg tggcgcagtg 120
accaacgcct cagaggctcc tacaagcgga tccccaggat cgcgcgcttc tccagaagtg 180
acaccactt ctaccctaa cccaaacaat gtcactcaga ataagaccac accaaccgag 240
cctgcaagtc ccctactac cccaagcct acaagtaetc caaaatcacc acccaccagc 300
acaccagacc ccaagcctaa aaacaataca actcccgcga agagcgggcg ccctacaaaa 360
cctccaggac cagtgtggtg cgaccggaga gatcccctgg ctcggtacgg atcaagagtg 420
cagatccgat gtcggttcag aaatagcaca aggatggagt ttcgcctgca gatctggcgg 480
tattccatgg gcccttctcc ccctattgcc ccagctcccg atctggagga agtgetgact 540
aacattaccg ctccaccggy cgggctgctg gtgtacgaca gtgcacccaa tctgaccgat 600
cctcacgtcc tgtgggcaga gggagcagga ccaggagcag accctccact gtatagcgtg 660
actggacctc tgccaaccca ggcctgatc attggagagg tgacaccagc cactcagggc 720
atgtactatc tggcttgggg gcgcatggat agccccacg aatacggcac atgggtgagg 780
gtccgcatgt tccggcccc ttcctgact ctgcagcctc atgcagtgat ggaggggagc 840
cccttcaagg ccacttgca cgcagccgct tactatccaa gaaaccccg ggagttcgtc 900
tggtttgaag acgataggca ggtgttcaat cctggacaga tcgacacaca gactcacgag 960
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cgcaacgcaa ccggactggc tctggtgctg ccaagaccta caatcactat ggagttcggc 1140
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ctgggggacg atccaagtcc cgcagccaaa tcagctgtga ccgcacagga gtccctgcgac 1260
caccaggac tggccacagt gagatctact ctgcccactt cttacgatta cagtgaatac 1320
atctgtaggc tgactggata tctgcggc atcccagtc tggagcacca tgggtcccat 1380
cagcctccac ccagagacc cacagaaagg caggtcatcg aggcattga atgggtcggg 1440
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agaacatctc agagtcgaca ggcacaccga cggagaggac gaaagaggcg ctccggggga 1560
gcccgtgcac gactgggagc cgtgatcctg ttcgtggtca ttgtgggect gcatggggtc 1620
aggggaaagt acgcaactggc cgacgcttct ctgaaaatgg ccgatcccaa tcggttccgg 1680

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ggcaaagacc tgcctgtgct ggaccagctg accgatcctc caggcgtgcg acgggtctat 1740
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tcatataaca aaagcctggg agcatgtcca atccgaacct agccacgggtg gaactactat 2040
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gaaaccgccc gaacatatct gaggtggtg aagatcaatg actggactga gatcaccagg 2160
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gctggagcag tgggaggcag cctgctggcc gccctggtca tctgcccgat tgtctattgg 2640
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gaccagccat cttcccacca gccactgttc tattga 2736

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<210> SEQ ID NO 91

<211> LENGTH: 901

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: pHSV2-gB amino acid sequence

<400> SEQUENCE: 91

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Met Arg Gly Gly Gly Leu Ile Cys Ala Leu Val Val Gly Ala Leu Val
1           5           10          15
Ala Ala Val Ala Ser Ala Ala Pro Ala Ala Pro Arg Ala Ser Gly Gly
20          25          30
Val Ala Ala Thr Val Ala Ala Asn Gly Gly Pro Ala Ser Gln Pro Pro
35          40          45
Pro Val Pro Ser Pro Ala Thr Thr Lys Ala Arg Lys Arg Lys Thr Lys
50          55          60
Lys Pro Pro Lys Arg Pro Glu Ala Thr Pro Pro Pro Asp Ala Asn Ala
65          70          75          80
Thr Val Ala Ala Gly His Ala Thr Leu Arg Ala His Leu Arg Glu Ile
85          90          95
Lys Val Glu Asn Ala Asp Ala Gln Phe Tyr Val Cys Pro Pro Pro Thr
100         105         110
Gly Ala Thr Val Val Gln Phe Glu Gln Pro Arg Arg Cys Pro Thr Arg
115         120         125
Pro Glu Gly Gln Asn Tyr Thr Glu Gly Ile Ala Val Val Phe Lys Glu
130         135         140
Asn Ile Ala Pro Tyr Lys Phe Lys Ala Thr Met Tyr Tyr Lys Asp Val
145         150         155         160
Thr Val Ser Gln Val Trp Phe Gly His Arg Tyr Ser Gln Phe Met Gly
165         170         175

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Ile Phe Glu Asp Arg Ala Pro Val Pro Phe Glu Glu Val Ile Asp Lys
180 185 190

Ile Asn Ala Lys Gly Val Cys Arg Ser Thr Ala Lys Tyr Val Arg Asn
195 200 205

Asn Met Glu Thr Thr Ala Phe His Arg Asp Asp His Glu Thr Asp Met
210 215 220

Glu Leu Lys Pro Ala Lys Val Ala Thr Arg Thr Ser Arg Gly Trp His
225 230 235 240

Thr Thr Asp Leu Lys Tyr Asn Pro Ser Arg Val Glu Ala Phe His Arg
245 250 255

Tyr Gly Thr Thr Val Asn Cys Ile Val Glu Glu Val Asp Ala Arg Ser
260 265 270

Val Tyr Pro Tyr Asp Glu Phe Val Leu Ala Thr Gly Asp Phe Val Tyr
275 280 285

Met Ser Pro Phe Tyr Gly Tyr Arg Glu Gly Ser His Thr Glu His Thr
290 295 300

Ser Tyr Ala Ala Asp Arg Phe Lys Gln Val Asp Gly Phe Tyr Ala Arg
305 310 315 320

Asp Leu Thr Thr Lys Ala Arg Ala Thr Ser Pro Thr Thr Arg Asn Leu
325 330 335

Leu Thr Thr Pro Lys Phe Thr Val Ala Trp Asp Trp Val Pro Lys Arg
340 345 350

Pro Ala Val Cys Thr Met Thr Lys Trp Gln Glu Val Asp Glu Met Leu
355 360 365

Arg Ala Glu Tyr Gly Gly Ser Phe Arg Phe Ser Ser Asp Ala Ile Ser
370 375 380

Thr Thr Phe Thr Thr Asn Leu Thr Glu Tyr Ser Leu Ser Arg Val Asp
385 390 395 400

Leu Gly Asp Cys Ile Gly Arg Asp Ala Arg Glu Ala Ile Asp Arg Met
405 410 415

Phe Ala Arg Lys Tyr Asn Ala Thr His Ile Lys Val Gly Gln Pro Gln
420 425 430

Tyr Tyr Leu Ala Thr Gly Gly Phe Leu Ile Ala Tyr Gln Pro Leu Leu
435 440 445

Ser Asn Thr Leu Ala Glu Leu Tyr Val Arg Glu Tyr Met Arg Glu Gln
450 455 460

Asp Arg Lys Pro Arg Asn Ala Thr Pro Ala Pro Leu Arg Glu Ala Pro
465 470 475 480

Ser Ala Asn Ala Ser Val Glu Arg Ile Lys Thr Thr Ser Ser Ile Glu
485 490 495

Phe Ala Arg Leu Gln Phe Thr Tyr Asn His Ile Gln Arg His Val Asn
500 505 510

Asp Met Leu Gly Arg Ile Ala Val Ala Trp Cys Glu Leu Gln Asn His
515 520 525

Glu Leu Thr Leu Trp Asn Glu Ala Arg Lys Leu Asn Pro Asn Ala Ile
530 535 540

Ala Ser Ala Thr Val Gly Arg Arg Val Ser Ala Arg Met Leu Gly Asp
545 550 555 560

Val Met Ala Val Ser Thr Cys Val Pro Val Ala Pro Asp Asn Val Ile
565 570 575

Val Gln Asn Ser Met Arg Val Ser Ser Arg Pro Gly Thr Cys Tyr Ser
580 585 590

Arg Pro Leu Val Ser Phe Arg Tyr Glu Asp Gln Gly Pro Leu Ile Glu

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595					600					605					
Gly	Gln	Leu	Gly	Glu	Asn	Asn	Glu	Leu	Arg	Leu	Thr	Arg	Asp	Ala	Leu
610					615					620					
Glu	Pro	Cys	Thr	Val	Gly	His	Arg	Arg	Tyr	Phe	Ile	Phe	Gly	Gly	Gly
625					630					635					640
Tyr	Val	Tyr	Phe	Glu	Glu	Tyr	Ala	Tyr	Ser	His	Gln	Leu	Ser	Arg	Ala
				645					650					655	
Asp	Val	Thr	Thr	Val	Ser	Thr	Phe	Ile	Asp	Leu	Asn	Ile	Thr	Met	Leu
				660					665					670	
Glu	Asp	His	Glu	Phe	Val	Pro	Leu	Glu	Val	Tyr	Thr	Arg	His	Glu	Ile
				675					680					685	
Lys	Asp	Ser	Gly	Leu	Leu	Asp	Tyr	Thr	Glu	Val	Gln	Arg	Arg	Asn	Gln
690						695					700				
Leu	His	Asp	Leu	Arg	Phe	Ala	Asp	Ile	Asp	Thr	Val	Ile	Arg	Ala	Asp
705					710					715					720
Ala	Asn	Ala	Ala	Met	Phe	Ala	Gly	Leu	Cys	Ala	Phe	Phe	Glu	Gly	Met
				725						730					735
Gly	Asp	Leu	Gly	Arg	Ala	Val	Gly	Lys	Val	Val	Met	Gly	Val	Val	Gly
				740					745					750	
Gly	Val	Val	Ser	Ala	Val	Ser	Gly	Val	Ser	Ser	Phe	Met	Ser	Asn	Pro
				755					760					765	
Phe	Gly	Ala	Leu	Ala	Val	Gly	Leu	Leu	Val	Leu	Ala	Gly	Leu	Val	Ala
770						775					780				
Ala	Phe	Phe	Ala	Phe	Arg	Tyr	Val	Leu	Gln	Leu	Gln	Arg	Asn	Pro	Met
785					790						795				800
Lys	Ala	Leu	Tyr	Pro	Leu	Thr	Thr	Lys	Glu	Leu	Lys	Thr	Ser	Asp	Pro
				805						810					815
Gly	Gly	Val	Gly	Gly	Glu	Gly	Glu	Glu	Gly	Ala	Glu	Gly	Gly	Gly	Phe
				820						825					830
Asp	Glu	Ala	Lys	Leu	Ala	Glu	Ala	Arg	Glu	Met	Ile	Arg	Tyr	Met	Ala
				835						840					845
Leu	Val	Ser	Ala	Met	Glu	Arg	Thr	Glu	His	Lys	Ala	Arg	Lys	Lys	Gly
850						855									860
Thr	Ser	Ala	Leu	Leu	Ser	Ser	Lys	Val	Thr	Asn	Met	Val	Leu	Arg	Lys
865						870									880
Arg	Asn	Lys	Ala	Arg	Tyr	Ser	Pro	Leu	His	Asn	Glu	Asp	Glu	Ala	Gly
				885						890					895
Asp	Glu	Asp	Glu	Leu											
				900											

<210> SEQ ID NO 92

<211> LENGTH: 2706

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: pHSV2-gB nucleic acid sequence

<400> SEQUENCE: 92

```

atgagaggcg gaggactgat ctgtgcactg gtcgtcggag cactgggcgc tgctgtcgca    60
tctgtgcccc ccgccgcacc ccgggccagc ggccgggttg cagctaccgt cgcagcaaac    120
ggaggcccag catctcagcc ccctccagtg ccaagtcccg ctaccacaaa ggcacgcaag    180
cgaaaaacca agaaccccc taaacgacca gaggcaacac caccocctga cgaaaacgct    240
actgtggctg caggacacgc caccctgcga gctcatctga gagagatcaa ggtcgaaaat    300

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gcagatgccc agttctacgt gtgcccaccc cctacaggag ccaactgtggt ccagtttgag	360
cagccccgga gatgtccaac tagaccogag gggcagaact acaccgaagg aatcgccgtg	420
gtcttcaagg aaaacatcgc accttacaag tttaaagcca caatgtacta caaagacgtg	480
actgtctccc aagtgtggtt cggccacaga tactctcagt tcatggggat tttgaggac	540
agggccccctg tgccatttga ggaagtcatc gataagatta atgcaaaagg cgtctgcaga	600
agcacagcca agtatgtgag gaacaatatg gaaactaccg ccttocacag ggacgatcat	660
gagactgaca tggaaactgaa gccagctaaa gtggcaacca ggacaagccg cggatggcac	720
acaactgatc tgaatacaaa cccctcccgg gtggaggcct tccatagata tggcaccaca	780
gtgaattgta tcgtggagga agtcgatgcc cgctccgtgt acccctatga cgaatttgtc	840
ctggctacog gcgatttctg gtacatgtct cctttttacg gatatagga gggcagccac	900
accgaacata catcctacgc cgctgaccgc ttcaagcagg tggatggggt ttatgcccg	960
gacctgacta ccaagcccg ggcaccacgc ccaacaactc gaaacctgct gaccacacct	1020
aagttcacag tggcttggga ctgggtccct aagcggccag cagtctgcac tatgacaaa	1080
tggcaggaag tggacgaat gctgcgagca gactacggcg gcagcttccg gttcagcagc	1140
gatgtatatt caactacott tacaactaat ctgaccgagt atagcctgtc cagagtggac	1200
ctgggggatt gtatcggacg agatgcccgg gaagctattg acaggatgtt cgcccgaag	1260
tacaacgcta ctcacatcaa agtgggccag cctcagtact atctggctac cggcgggttt	1320
ctgattgcat atcagccact gctgtccaat acaactggccg agctgtacgt gcgagagtat	1380
atgcgggaac aggacagaaa gccaaaggac gcaaccccag cccctctgcg agaagcacc	1440
tcagccaatg ctagcgtgga gcggatcaaaa accacatcta gtattgaatt cgctagactg	1500
cagtttacot acaaccacat ccagagacat gtcaatgata tgctgggcag gattgcagtg	1560
gcctggtgcg agctgcagaa ccatgaactg actctgtgga atgaggcccg gaagctgaac	1620
cctaattgcta tcgcatcagc caccgtgggc cggcgggtga gcgccagaat gctgggcgac	1680
gtgatggcag tctctacatg cgtgccgctc gccctgata acgtgattgt ccagaatagt	1740
atgagagtgt caagcaggcc tggcacctgt tacagtaggc cactggtgct attccgctat	1800
gaagaccagg gacctctgat cgagggacag ctgggagaga acaatgaact gcgcctgaca	1860
cgagatgccc tggagccatg cactgtgggc caccgacggt atttcatttt tggagggggg	1920
tacgtgtatt tcgaggaata cgcttattcc catcagctgt ctagggcaga cgtgactacc	1980
gtcagtacct tcctcgacct gaacattaca atgctggagg atcacgaatt tgtgccctg	2040
gaggtctaca cacgccatga aatcaaggac agcggactgc tggattatac tgaggtgcag	2100
agaaggaacc agctgcacga cctgcgcttc gccgacatcg atacagtgat tcgggctgat	2160
gcaaatgcag ccatgtttgc aggcctgtgc gccttctttg agggaaatggg cgatctggga	2220
cgagcagtgg ggaagtggt catgggggtg gtcggaggcg tggctctctg tgtgagtgga	2280
gtctcctctt tcatgagcaa cctttttgga gccctggctg tgggactgct ggtcctggca	2340
ggcctggtgg ccgcattctt tgctttcaga tacgtgctgc agctgcagag gaatccaatg	2400
aaggccctgt atcccctgac aactaaggag ctgaaaaacct ccgaccacgg gggagtgggc	2460
ggggagggag aggaaggggc agagggcggc ggctttgatg aggcmaaagct ggagaggcc	2520
cgcgaaatga tccgatacat ggctctggtg tcagcaatgg agcgaaccga acacaaagcc	2580
cggaagaaag gcaccagcgc cctgctgagt tcaaaagtga ctaacatggt cctgcggaaa	2640
agaaacaaag cccgctattc cccactgcat aatgaggatg aagccggcga ttaggacgaa	2700

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ctgtga

2706

<210> SEQ ID NO 93
 <211> LENGTH: 1068
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: pHSV2-gHgL amino acid sequence

<400> SEQUENCE: 93

```

Met Gly Pro Gly Leu Trp Val Val Met Gly Val Leu Val Gly Val Ala
 1          5          10          15
Gly Gly His Asp Thr Tyr Trp Thr Glu Gln Ile Asp Pro Trp Phe Leu
 20          25          30
His Gly Leu Gly Leu Ala Arg Thr Tyr Trp Arg Asp Thr Asn Thr Gly
 35          40          45
Arg Leu Trp Leu Pro Asn Thr Pro Asp Ala Ser Asp Pro Gln Arg Gly
 50          55          60
Arg Leu Ala Pro Pro Gly Glu Leu Asn Leu Thr Thr Ala Ser Val Pro
 65          70          75          80
Met Leu Arg Trp Tyr Ala Glu Arg Phe Cys Phe Val Leu Val Thr Thr
 85          90          95
Ala Glu Phe Pro Arg Asp Pro Gly Gln Leu Leu Tyr Ile Pro Lys Thr
 100         105         110
Tyr Leu Leu Gly Arg Pro Arg Asn Ala Ser Leu Pro Glu Leu Pro Glu
 115         120         125
Ala Gly Pro Thr Ser Arg Pro Pro Ala Glu Val Thr Gln Leu Lys Gly
 130         135         140
Leu Ser His Asn Pro Gly Ala Ser Ala Leu Leu Arg Ser Arg Ala Trp
 145         150         155         160
Val Thr Phe Ala Ala Ala Pro Asp Arg Glu Gly Leu Thr Phe Pro Arg
 165         170         175
Gly Asp Asp Gly Ala Thr Glu Arg His Pro Asp Gly Arg Arg Asn Ala
 180         185         190
Pro Pro Pro Gly Pro Pro Ala Gly Thr Pro Arg His Pro Thr Thr Asn
 195         200         205
Leu Ser Ile Ala His Leu His Asn Ala Ser Val Thr Trp Leu Ala Ala
 210         215         220
Arg Gly Leu Leu Arg Thr Pro Gly Arg Tyr Val Tyr Leu Ser Pro Ser
 225         230         235         240
Ala Ser Thr Trp Pro Val Gly Val Trp Thr Thr Gly Gly Leu Ala Phe
 245         250         255
Gly Cys Asp Ala Ala Leu Val Arg Ala Arg Tyr Gly Lys Gly Phe Met
 260         265         270
Gly Leu Val Ile Ser Met Arg Asp Ser Pro Pro Ala Glu Ile Ile Val
 275         280         285
Val Pro Ala Asp Lys Thr Leu Ala Arg Val Gly Asn Pro Thr Asp Glu
 290         295         300
Asn Ala Pro Ala Val Leu Pro Gly Pro Pro Ala Gly Pro Arg Tyr Arg
 305         310         315         320
Val Phe Val Leu Gly Ala Pro Thr Pro Ala Asp Asn Gly Ser Ala Leu
 325         330         335
Asp Ala Leu Arg Arg Val Ala Gly Tyr Pro Glu Glu Ser Thr Asn Tyr
 340         345         350

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Ala Gln Tyr Met Ser Arg Ala Tyr Ala Glu Phe Leu Gly Glu Asp Pro
355 360 365

Gly Ser Gly Thr Asp Ala Arg Pro Ser Leu Phe Trp Arg Leu Ala Gly
370 375 380

Leu Leu Ala Ser Ser Gly Phe Ala Phe Val Asn Ala Ala His Ala His
385 390 395 400

Asp Ala Ile Arg Leu Ser Asp Leu Leu Gly Phe Leu Ala His Ser Arg
405 410 415

Val Leu Ala Gly Leu Ala Ala Arg Gly Ala Ala Gly Cys Ala Ala Asp
420 425 430

Ser Val Phe Leu Asn Val Ser Val Leu Asp Pro Ala Ala Arg Leu Arg
435 440 445

Leu Glu Ala Arg Leu Gly His Leu Val Ala Ala Ile Leu Glu Arg Glu
450 455 460

Gln Ser Leu Val Ala His Ala Leu Gly Tyr Gln Leu Ala Phe Val Leu
465 470 475 480

Asp Ser Pro Ala Ala Tyr Gly Ala Val Ala Pro Ser Ala Ala Arg Leu
485 490 495

Ile Asp Ala Leu Tyr Ala Glu Phe Leu Gly Gly Arg Ala Leu Thr Ala
500 505 510

Pro Met Val Arg Arg Ala Leu Phe Tyr Ala Thr Ala Val Leu Arg Ala
515 520 525

Pro Phe Leu Ala Gly Ala Pro Ser Ala Glu Gln Arg Glu Arg Ala Arg
530 535 540

Arg Gly Leu Leu Ile Thr Thr Ala Leu Cys Thr Ser Asp Val Ala Ala
545 550 555 560

Ala Thr His Ala Asp Leu Arg Ala Ala Leu Ala Arg Thr Asp His Gln
565 570 575

Lys Asn Leu Phe Trp Leu Pro Asp His Phe Ser Pro Cys Ala Ala Ser
580 585 590

Leu Arg Phe Asp Leu Ala Glu Gly Gly Phe Ile Leu Asp Ala Leu Ala
595 600 605

Met Ala Thr Arg Ser Asp Ile Pro Ala Asp Val Met Ala Gln Gln Thr
610 615 620

Arg Gly Val Ala Ser Val Leu Thr Arg Trp Ala His Tyr Asn Ala Leu
625 630 635 640

Ile Arg Ala Phe Val Pro Glu Ala Thr His Gln Cys Ser Gly Pro Ser
645 650 655

His Asn Ala Glu Pro Arg Ile Leu Val Pro Ile Thr His Asn Ala Ser
660 665 670

Tyr Val Val Thr His Thr Pro Leu Pro Arg Gly Ile Gly Tyr Lys Leu
675 680 685

Thr Gly Val Asp Val Arg Arg Pro Leu Phe Ile Thr Tyr Leu Thr Ala
690 695 700

Thr Cys Glu Gly His Ala Arg Glu Ile Glu Pro Lys Arg Leu Val Arg
705 710 715 720

Thr Glu Asn Arg Arg Asp Leu Gly Leu Val Gly Ala Val Phe Leu Arg
725 730 735

Tyr Thr Pro Ala Gly Glu Val Met Ser Val Leu Leu Val Asp Thr Asp
740 745 750

Ala Thr Gln Gln Gln Leu Ala Gln Gly Pro Val Ala Gly Thr Pro Asn
755 760 765

Val Phe Ser Ser Asp Val Pro Ser Val Ala Leu Leu Leu Phe Pro Asn

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770	775	780
Gly Thr Val Ile His Leu	Leu Ala Phe Asp Thr	Leu Pro Ile Ala Thr
785	790	795 800
Ile Ala Pro Gly Phe Leu	Ala Ala Ser Ala Leu	Gly Val Val Met Ile
	805	810 815
Thr Ala Ala Leu Ala Gly	Ile Leu Arg Val Val	Arg Thr Cys Val Pro
	820	825 830
Phe Leu Trp Arg Arg Glu	Arg Gly Arg Lys Arg	Arg Ser Gly Phe Val
	835	840 845
Cys Leu Phe Gly Leu Val	Val Met Gly Ala Trp	Gly Ala Trp Gly Gly
	850	855 860
Ser Gln Ala Thr Glu Tyr	Val Leu Arg Ser Val	Ile Ala Lys Glu Val
865	870	875 880
Gly Asp Ile Leu Arg Val	Pro Cys Met Arg Thr	Pro Ala Asp Asp Val
	885	890 895
Ser Trp Arg Tyr Glu Ala	Pro Ser Val Ile Asp	Tyr Ala Arg Ile Asp
	900	905 910
Gly Ile Phe Leu Arg Tyr	His Cys Pro Gly Leu	Asp Thr Phe Leu Trp
	915	920 925
Asp Arg His Ala Gln Arg	Ala Tyr Leu Val Asn	Pro Phe Leu Phe Ala
	930	935 940
Ala Gly Phe Leu Glu Asp	Leu Ser His Ser Val	Phe Pro Ala Asp Thr
	945	950 955 960
Gln Glu Thr Thr Thr Arg	Arg Ala Leu Tyr Lys	Glu Ile Arg Asp Ala
	965	970 975
Leu Gly Ser Arg Lys Gln	Ala Val Ser His Ala	Pro Val Arg Ala Gly
	980	985 990
Cys Val Asn Phe Asp Tyr	Ser Arg Thr Arg Arg	Cys Val Gly Arg Arg
	995	1000 1005
Asp Leu Arg Pro Ala Asn	Thr Thr Ser Thr Trp	Glu Pro Pro Val
	1010	1015 1020
Ser Ser Asp Asp Glu Ala	Ser Ser Gln Ser Lys	Pro Leu Ala Thr
	1025	1030 1035
Gln Pro Pro Val Leu Ala	Leu Ser Asn Ala Pro	Pro Arg Arg Val
	1040	1045 1050
Ser Pro Thr Arg Gly Arg	Arg Arg His Thr Arg	Leu Arg Arg Asn
	1055	1060 1065

<210> SEQ ID NO 94

<211> LENGTH: 3207

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: pHSV2-gHgL nucleic acid sequence

<400> SEQUENCE: 94

```

atggggcctg gactgtgggt cgtgatggga gtgctggtcg gcgtggctgg agggcatgat   60
acatactgga ctgaacagat tgatccttgg tttctgcatg gactgggcct ggccaggaca   120
tactggcgcg acaccaacac aggcaggctg tggctgcccc atactcctga cgcatctgat   180
ccacagaggg gccgcctggc tccccctgga gagctgaacc tgaccacagc aagtgtgccc   240
atgctgcatg ggtatgctga gcggttctgc tttgtgctgg tcactaccgc cgaattccca   300
agggatcccg gccagctgct gtacatcccc aagacctatc tgctggggcg acctcgaaac   360
gcctcactgc ctgagctgcc agaagctgga cctaccagcc gccaccgccg agaggtgaca   420

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cagctgaaag gactgagcca caatecagge gcctctgctc tgctgagaag tagggcctgg	480
gtgaccttcg ccgctgcacc agaccgagag ggactgacct ttccccgggg cgacgatgga	540
gccacagaaa gacaccctga tgggcgagaga aatgcccctc caccocggcc tccagctgga	600
acccccaggc atcctacaac taacctgtca atcgcccacc tgcataatgc tagcgtgact	660
tggctggcag ccagaggcct gctgcgaacc ccaggaagat acgtgtatct gagtccctca	720
gccagcacct ggctgtggg agtctggacc acaggcgggc tggccttcgg ctgtgacgca	780
gccctggtgc gcgctcgata cgggaagggc ttcattgggc tggtcattag catgagagat	840
agccctcccg ccgagatcat tgtggtccc gcagacaaaa ctctggccag ggtggggaac	900
cctaccgatg aaaatgcacc agccgtcctg ccaggaccac ccgaggacc acggtataga	960
gtgtttgtcc tgggagctcc aactcccga gacaacggct ccgcactgga tgcactgagg	1020
cgctggcag gataccaga ggaatccacc aattacgctc agtatatgtc tcgggcttat	1080
gcagagtcc tgggagaaga ccttgaagc ggaacagatg cacgaccatc cctgttttgg	1140
agactggcag gactgctggc tagctccgga ttcgctttg tgaacgctgc acacgctcat	1200
gacgcaatca gactgagtga tctgctgggg ttcctggcac actcacgctg gctggctgga	1260
ctggcagctc gggcgcgagc aggatcgct gcagactccg tgtttctgaa cgtgagcgtg	1320
ctggatccag cagctaggct gcgactggag gcaagactgg gacacctggt ggcagccatc	1380
ctggagaggg aacagagcct ggtcgcccat gctctgggt accagctggc cttcgtgctg	1440
gactctcccg ctgcatatgg agcagtcgca cctagtcccg ctgactgat tgatgcctg	1500
tacgctgaat ttctgggagg ccgggcactg accgcacctg tggcgcgacg ggcctgttc	1560
tatgctacag cagtcctgag cgctccattt ctggcaggag ctccatccgc agagcagcga	1620
gaacgagcaa gaaggggcct gctgatcact accgcccgt gcacatctga cgtggcagcc	1680
gctactcaag cagatctgag agcagccctg gccaggaccg accaccagaa gaacctgttc	1740
tggctgcctg atcatttttc accatgtgct gcaagcctgc gattogacct ggcagagggc	1800
ggcttcctcc tggatgcaact ggccatggct acacggagtg acattcccgc agatgtgatg	1860
gcccagcaga caagaggagt ggccctcagtc ctgactagat gggctcatta caatgcactg	1920
atccgcgct tcgtgcctga ggccacacac cagtgcagtg ggccatcaca taacgctgaa	1980
ccccggatcc tgggtcctat tactcacaat gcctcctacg tggcactca taccctctg	2040
ccaagaggaa ttggctataa gctgacagga gtggacgtgc gggggcccct gttcactact	2100
tacctgacag ctacttgtga gggccacgca agggagattg aacaaaaacg cctggtgca	2160
accgaaaacc ggagagatct gggactggtg ggcgcctct ttctgcgcta tacaccgct	2220
ggcgaagtga tgagcgtgct gctggtcgac accgatgcca cacagcagca gctggctcag	2280
ggaccagtgg caggaacccc caacgtcttc tctagtacg tgccaagcgt ggcctgctg	2340
ctgttcccga atggcacagt gatccacctg ctggcctttg atactctgcc tatoctacc	2400
attgcaccag ggttcctggc agcttcggcc ctgggagtg tcatgatcac tgcagccctg	2460
gcaggaatc tgcgagtggt cagaacctgc gtgcctttc tgtggaggcg cgagagagga	2520
aggaagcgac ggtctggtc cgtgtgctg tttggcctgg tggcattggg agcatgggga	2580
gcttggggcg ggagccaggc aactgagtae gtccctgggt ccgtgatcgc taaagaagtg	2640
ggcgacatc tgcgctccc ttgcatgca acaccagccg acgacgtgag ctggagatac	2700
gaggctccca gtgtcatoga ctatgcaaga atcgatggca ttttctgag gtaccactgt	2760

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ctctggctgg acaccttct gtgggatagg catgcacagc ggcctatct ggtgaacca 2820
ttcctgtttg ctgcaggctt cctggaagac ctgtcccaca gcgtgttccc cgccgataca 2880
caggagacaa ctaccagaag ggcactgtac aaggaaatta gggacgcctt gggcagtcgc 2940
aaacaggctg tctcacatgc acccgtgcgc gcaggatgcg tcaacttcga ctatagccgg 3000
actcggcggg gcgtgggacg gagagatctg aggcccgcca atacaacttc cacctgggag 3060
cctccagtgt caagcgacga tgaggccagc agccagtcca aacctctggc aaccagccc 3120
cctgtgctgg ctctgtctaa tgcaccacc cgaagagtct cacctacaag aggacggcga 3180
cgacataccc gcctgcgacg gaattga 3207

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<210> SEQ ID NO 95

<211> LENGTH: 879

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: pHSV2-gCgD amino acid sequence

<400> SEQUENCE: 95

```

Met Ala Leu Gly Arg Val Gly Leu Ala Val Gly Leu Trp Gly Leu Leu
1           5           10           15
Trp Val Gly Val Val Val Val Leu Ala Asn Ala Ser Pro Gly Arg Thr
20           25           30
Ile Thr Val Gly Pro Arg Gly Asn Ala Ser Asn Ala Ala Pro Ser Ala
35           40           45
Ser Pro Arg Asn Ala Ser Ala Pro Arg Thr Thr Pro Thr Pro Pro Gln
50           55           60
Pro Arg Lys Ala Thr Lys Ser Lys Ala Ser Thr Ala Lys Pro Ala Pro
65           70           75           80
Pro Pro Lys Thr Gly Pro Pro Lys Thr Ser Ser Glu Pro Val Arg Cys
85           90           95
Asn Arg His Asp Pro Leu Ala Arg Tyr Gly Ser Arg Val Gln Ile Arg
100          105          110
Cys Arg Phe Pro Asn Ser Thr Arg Thr Glu Phe Arg Leu Gln Ile Trp
115          120          125
Arg Tyr Ala Thr Ala Thr Asp Ala Glu Ile Gly Thr Ala Pro Ser Leu
130          135          140
Glu Glu Val Met Val Asn Val Ser Ala Pro Pro Gly Gly Gln Leu Val
145          150          155          160
Tyr Asp Ser Ala Pro Asn Arg Thr Asp Pro His Val Ile Trp Ala Glu
165          170          175
Gly Ala Gly Pro Gly Ala Ser Pro Arg Leu Tyr Ser Val Val Gly Pro
180          185          190
Leu Gly Arg Gln Arg Leu Ile Ile Glu Glu Leu Thr Leu Glu Thr Gln
195          200          205
Gly Met Tyr Tyr Trp Val Trp Gly Arg Thr Asp Arg Pro Ser Ala Tyr
210          215          220
Gly Thr Trp Val Arg Val Arg Val Phe Arg Pro Pro Ser Leu Thr Ile
225          230          235          240
His Pro His Ala Val Leu Glu Gly Gln Pro Phe Lys Ala Thr Cys Thr
245          250          255
Ala Ala Thr Tyr Tyr Pro Gly Asn Arg Ala Glu Phe Val Trp Phe Glu
260          265          270
Asp Gly Arg Arg Val Phe Asp Pro Ala Gln Ile His Thr Gln Thr Gln
275          280          285

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Glu Asn Pro Asp Gly Phe Ser Thr Val Ser Thr Val Thr Ser Ala Ala
 290 295 300
 Val Gly Gly Gln Gly Pro Pro Arg Thr Phe Thr Cys Gln Leu Thr Trp
 305 310 315 320
 His Arg Asp Ser Val Ser Phe Ser Arg Arg Asn Ala Ser Gly Thr Ala
 325 330 335
 Ser Val Leu Pro Arg Pro Thr Ile Thr Met Glu Phe Thr Gly Asp His
 340 345 350
 Ala Val Cys Thr Ala Gly Cys Val Pro Glu Gly Val Thr Phe Ala Trp
 355 360 365
 Phe Leu Gly Asp Asp Ser Ser Pro Ala Glu Lys Val Ala Val Ala Ser
 370 375 380
 Gln Thr Ser Cys Gly Arg Pro Gly Thr Ala Thr Ile Arg Ser Thr Leu
 385 390 395 400
 Pro Val Ser Tyr Glu Gln Thr Glu Tyr Ile Cys Arg Leu Ala Gly Tyr
 405 410 415
 Pro Asp Gly Ile Pro Val Leu Glu His His Gly Ser His Gln Pro Pro
 420 425 430
 Pro Arg Asp Pro Thr Glu Arg Gln Val Ile Arg Ala Val Glu Gly Ala
 435 440 445
 Gly Ile Gly Val Ala Val Leu Val Ala Val Val Leu Ala Gly Thr Ala
 450 455 460
 Val Val Tyr Leu Thr His Ala Ser Ser Val Arg Tyr Arg Arg Leu Arg
 465 470 475 480
 Arg Gly Arg Lys Arg Arg Ser Gly Arg Leu Thr Ser Gly Val Gly Thr
 485 490 495
 Ala Ala Leu Leu Val Val Ala Val Gly Leu Arg Val Val Cys Ala Lys
 500 505 510
 Tyr Ala Leu Ala Asp Pro Ser Leu Lys Met Ala Asp Pro Asn Arg Phe
 515 520 525
 Arg Gly Lys Asn Leu Pro Val Leu Asp Gln Leu Thr Asp Pro Pro Gly
 530 535 540
 Val Lys Arg Val Tyr His Ile Gln Pro Ser Leu Glu Asp Pro Phe Gln
 545 550 555 560
 Pro Pro Ser Ile Pro Ile Thr Val Tyr Tyr Ala Val Leu Glu Arg Ala
 565 570 575
 Cys Arg Ser Val Leu Leu His Ala Pro Ser Glu Ala Pro Gln Ile Val
 580 585 590
 Arg Gly Ala Ser Asp Glu Ala Arg Lys His Thr Tyr Asn Leu Thr Ile
 595 600 605
 Ala Trp Tyr Arg Met Gly Asp Asn Cys Ala Ile Pro Ile Thr Val Met
 610 615 620
 Glu Tyr Thr Glu Cys Pro Tyr Asn Lys Ser Leu Gly Val Cys Pro Ile
 625 630 635 640
 Arg Thr Gln Pro Arg Trp Ser Tyr Tyr Asp Ser Phe Ser Ala Val Ser
 645 650 655
 Glu Asp Asn Leu Gly Phe Leu Met His Ala Pro Ala Phe Glu Thr Ala
 660 665 670
 Gly Thr Tyr Leu Arg Leu Val Lys Ile Asn Asp Trp Thr Glu Ile Thr
 675 680 685
 Gln Phe Ile Leu Glu His Arg Ala Arg Ala Ser Cys Lys Tyr Ala Leu
 690 695 700

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Pro Leu Arg Ile Pro Pro Ala Ala Cys Leu Thr Ser Lys Ala Tyr Gln
705 710 715 720

Gln Gly Val Thr Val Asp Ser Ile Gly Met Leu Pro Arg Phe Ile Pro
725 730 735

Glu Asn Gln Arg Thr Val Ala Leu Tyr Ser Leu Lys Ile Ala Gly Trp
740 745 750

His Gly Pro Lys Pro Pro Tyr Thr Ser Thr Leu Leu Pro Pro Glu Leu
755 760 765

Ser Asp Thr Thr Asn Ala Thr Gln Pro Glu Leu Val Pro Glu Asp Pro
770 775 780

Glu Asp Ser Ala Leu Leu Glu Asp Pro Ala Gly Thr Val Ser Ser Gln
785 790 795 800

Ile Pro Pro Asn Trp His Ile Pro Ser Ile Gln Asp Val Ala Pro His
805 810 815

His Ala Pro Ala Ala Pro Ser Asn Pro Gly Leu Ile Ile Gly Ala Leu
820 825 830

Ala Gly Ser Thr Leu Ala Val Leu Val Ile Gly Gly Ile Ala Phe Trp
835 840 845

Val Arg Arg Arg Ala Gln Met Ala Pro Lys Arg Leu Arg Leu Pro His
850 855 860

Ile Arg Asp Asp Asp Ala Pro Pro Ser His Gln Pro Leu Phe Tyr
865 870 875

<210> SEQ ID NO 96

<211> LENGTH: 2640

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: pHSV2-gCgD nucleic acid sequence

<400> SEQUENCE: 96

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atggcactgg gaagggtcgg gctggctgtc gggctgtggg ggctgctgtg ggtcggagtg      60
gtcgtggtcc tggctaatgc aagtcaggc agaacaatca ctgtgggacc caggggcaac      120
gctagtaatg ccgctccaag tgcatacccc aggaacgcct cagctcctcg caccacacca      180
acctctcccc agcctagaaa ggccactaag agcaaagcat ccaccgcaa accagctcca      240
ccccctaaga ctggaccacc caaaaccagc tccgagcccc tgcgctgcaa ccgacacgac      300
cctctggcac gatacggctc acgggtgcag atccgctgtc gattccctaa tagcaccaga      360
acagagttta ggctgcagat ctggagatat gcaactgcca ccgatgctga aattggcacc      420
gcaccaagtc tggaggaagt gatggtcaac gtgtcagctc ctccaggcgg gcagctggtc      480
tacgacagcg ccccaaatcg cacagatccc catgtgatct gggcagaggg agcaggacca      540
ggagcaagtc ctcggtgta ttcagtggc ggaccactgg gacggcagag actgatcatt      600
gaggaactga ccctgaaac acaggggatg tactattggg tgtggggacg gactgacaga      660
ccttctgctc acggaacctg ggtcagggtg cgcgtcttca gacccctag tctgacaatc      720
caccacatg ccgtgctgga gggacagccc tttaaggcta catgcactgc agccacttac      780
tatccggaa acagggctga gttcgtctgg tttgaagacg gccggagagt gttcgatcca      840
gccagattc acaccagac acaggaanaat cccgatggat tttctaccgt cagtactgtg      900
acctccgctg cagtgggagg ccagggcca cccagaacat tcaactgtca gctgacttgg      960
cacagggaca gcgtctcctt ttctagggc aatgcatccg ggaccgcctc tgtgctgcct     1020
agaccaacca tcacaatgga gttcaccgga gatcatgccg tgtgcacagc aggctgcgtg     1080

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cccgaagggg tgacctgcg tggtttctg ggcgacgatt ctagtctgc cgagaaggtg 1140
gtgtgcat cacagacaag ctgcgccgc cctggaactg caaccattcg aagcacactg 1200
ccagtgtcct acgagcagac tgaatatatc tgtagactgg ccgggtaccc agacggaatt 1260
cccgtgctgg agcaccatgg atcccaccag cctccacca gggatccaac cgagcgacag 1320
gtcatccgag cagtggaagg agctgggatt ggagtggcag tcctgggtggc cgtggctctg 1380
gctggaacag cagtggctca cctgactcat gcctcaagcg tgcgctatcg acggctgaga 1440
aggggacgaa aacgccgatc tggccggctg acaagtggag tcggaactgc cgccctgctg 1500
gtcgtggcag tgggactgcg agtggctctgc gcaaagtacg cactggctga cccaagcctg 1560
aaaatggcgg atcccaccg attccggggc aagaatctgc cagtgtgga ccagctgacc 1620
gatcctccag gggtcaaacg cgtgtatcac atccagccta gcctggagga cccatttcag 1680
ccccctcca tcccattac agtctactat gccgtgctgg aaagggcttg ccgctcagtc 1740
ctgctgcacg ctctagcga ggcaccacag atcgtgagag gcgccagcga cgaagctagg 1800
aagcatacct acaacctgac aattgcatgg tatcggatgg gggataattg tgccatcccc 1860
attaccgtga tggagtacac agaatgccct tataacaaaa gcctgggctg gtgccaatc 1920
cgaaccacgc ctagatggtc ttactatgac agtttctcag ccgtgagtga ggataacctg 1980
gggttcctga tgcacgcacc tgcctttgaa actgccggaa cctacctgcg cctggtgaag 2040
atcaatgact ggacagagat cactcagttt attctggaac atagagctag ggcatcctgc 2100
aagtacgctc tgccactgcg gattccaccc gcagcctgctc tgacctcaa agcctatcag 2160
cagggcgctc cagtggattc tatcgggatg ctgccccgct tcattcctga gaaccagcgg 2220
accgtggccc tgtactctct gaagatcgtc ggatggcagc gccctaaacc tccatataca 2280
tccactctgc tgccccctga gctgtctgac actaccaatg ccactcagcc agaactggtg 2340
cccgaggacc ctgaagattc cgcactgctg gaggaccag caggaacagt gtcctctcag 2400
attccacca actggcatat cctttctatt caggatgtgg caccacacca tgccccagct 2460
gcaccagca atcctggcct gatcattggg gccctggctg gatccacct ggccgtgctg 2520
gtcatcggcg gcattgcatt ttgggtgcgg agaagggccc agatggctcc caagcggctg 2580
cgctgcccc atattagaga cgacgacgct cctccatccc accagccact gttttactga 2640

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<210> SEQ ID NO 97

<211> LENGTH: 931

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: pVZV-gB amino acid sequence

<400> SEQUENCE: 97

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Met Ser Pro Cys Gly Tyr Tyr Ser Lys Trp Arg Asn Arg Asp Arg Pro
1           5           10           15

Glu Tyr Arg Arg Asn Leu Arg Phe Arg Arg Phe Phe Ser Ser Ile His
                20           25           30

Pro Asn Ala Ala Ala Gly Ser Gly Phe Asn Gly Pro Gly Val Phe Ile
            35           40           45

Thr Ser Val Thr Gly Val Trp Leu Cys Phe Leu Cys Ile Phe Ser Met
            50           55           60

Phe Val Thr Ala Val Val Ser Val Ser Pro Ser Ser Phe Tyr Glu Ser
65           70           75           80

Leu Gln Val Glu Pro Thr Gln Ser Glu Asp Ile Thr Arg Ser Ala His
            85           90           95

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Leu Gly Asp Gly Asp Glu Ile Arg Glu Ala Ile His Lys Ser Gln Asp
 100 105 110
 Ala Glu Thr Lys Pro Thr Phe Tyr Val Cys Pro Pro Pro Thr Gly Ser
 115 120 125
 Thr Ile Val Arg Leu Glu Pro Thr Arg Thr Cys Pro Asp Tyr His Leu
 130 135 140
 Gly Lys Asn Phe Thr Glu Gly Ile Ala Val Val Tyr Lys Glu Asn Ile
 145 150 155 160
 Ala Ala Tyr Lys Phe Lys Ala Thr Val Tyr Tyr Lys Asp Val Ile Val
 165 170 175
 Ser Thr Ala Trp Ala Gly Ser Ser Tyr Thr Gln Ile Thr Asn Arg Tyr
 180 185 190
 Ala Asp Arg Val Pro Ile Pro Val Ser Glu Ile Thr Asp Thr Ile Asp
 195 200 205
 Lys Phe Gly Lys Cys Ser Ser Lys Ala Thr Tyr Val Arg Asn Asn His
 210 215 220
 Lys Val Glu Ala Phe Asn Glu Asp Lys Asn Pro Gln Asp Met Pro Leu
 225 230 235 240
 Ile Ala Ser Lys Tyr Asn Ser Val Gly Ser Lys Ala Trp His Thr Thr
 245 250 255
 Asn Asp Thr Tyr Met Val Ala Gly Thr Pro Gly Thr Tyr Arg Thr Gly
 260 265 270
 Thr Ser Val Asn Cys Ile Ile Glu Glu Val Glu Ala Arg Ser Ile Phe
 275 280 285
 Pro Tyr Asp Ser Phe Gly Leu Ser Thr Gly Asp Ile Ile Tyr Met Ser
 290 295 300
 Pro Phe Phe Gly Leu Arg Asp Gly Ala Tyr Arg Glu His Ser Asn Tyr
 305 310 315 320
 Ala Met Asp Arg Phe His Gln Phe Glu Gly Tyr Arg Gln Arg Asp Leu
 325 330 335
 Asp Thr Arg Ala Leu Leu Glu Pro Ala Ala Arg Asn Phe Leu Val Thr
 340 345 350
 Pro His Leu Thr Val Gly Trp Asn Trp Lys Pro Lys Arg Thr Glu Val
 355 360 365
 Cys Ser Leu Val Lys Trp Arg Glu Val Glu Asp Val Val Arg Asp Glu
 370 375 380
 Tyr Ala His Asn Phe Arg Phe Thr Met Lys Thr Leu Ser Thr Thr Phe
 385 390 395 400
 Ile Ser Glu Thr Asn Glu Phe Asn Leu Asn Gln Ile His Leu Ser Gln
 405 410 415
 Cys Val Lys Glu Glu Ala Arg Ala Ile Ile Asn Arg Ile Tyr Thr Thr
 420 425 430
 Arg Tyr Asn Ser Ser His Val Arg Thr Gly Asp Ile Gln Thr Tyr Leu
 435 440 445
 Ala Arg Gly Gly Phe Val Val Val Phe Gln Pro Leu Leu Ser Asn Ser
 450 455 460
 Leu Ala Arg Leu Tyr Leu Gln Glu Leu Val Arg Glu Asn Thr Asn His
 465 470 475 480
 Ser Pro Gln Lys His Pro Thr Arg Asn Thr Arg Ser Arg Arg Ser Val
 485 490 495
 Pro Val Glu Leu Arg Ala Asn Arg Thr Ile Thr Thr Thr Ser Ser Val
 500 505 510

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Glu Phe Ala Met Leu Gln Phe Thr Tyr Asp His Ile Gln Glu His Val
 515 520 525
 Asn Glu Met Leu Ala Arg Ile Ser Ser Ser Trp Cys Gln Leu Gln Asn
 530 535 540
 Arg Glu Arg Ala Leu Trp Ser Gly Leu Phe Pro Ile Asn Pro Ser Ala
 545 550 555 560
 Leu Ala Ser Thr Ile Leu Asp Gln Arg Val Lys Ala Arg Ile Leu Gly
 565 570 575
 Asp Val Ile Ser Val Ser Asn Cys Pro Glu Leu Gly Ser Asp Thr Arg
 580 585 590
 Ile Ile Leu Gln Asn Ser Met Arg Val Ser Gly Ser Thr Thr Arg Cys
 595 600 605
 Tyr Ser Arg Pro Leu Ile Ser Ile Val Ser Leu Asn Gly Ser Gly Thr
 610 615 620
 Val Glu Gly Gln Leu Gly Thr Asp Asn Glu Leu Ile Met Ser Arg Asp
 625 630 635 640
 Leu Leu Glu Pro Cys Val Ala Asn His Lys Arg Tyr Phe Leu Phe Gly
 645 650 655
 His His Tyr Val Tyr Tyr Glu Asp Tyr Arg Tyr Val Arg Glu Ile Ala
 660 665 670
 Val His Asp Val Gly Met Ile Ser Thr Tyr Val Asp Leu Asn Leu Thr
 675 680 685
 Leu Leu Lys Asp Arg Glu Phe Met Pro Leu Gln Val Tyr Thr Arg Asp
 690 695 700
 Glu Leu Arg Asp Thr Gly Leu Leu Asp Tyr Ser Glu Ile Gln Arg Arg
 705 710 715 720
 Asn Gln Met His Ser Leu Arg Phe Tyr Asp Ile Asp Lys Val Val Gln
 725 730 735
 Tyr Asp Ser Gly Thr Ala Ile Met Gln Gly Met Ala Gln Phe Phe Gln
 740 745 750
 Gly Leu Gly Thr Ala Gly Gln Ala Val Gly His Val Val Leu Gly Ala
 755 760 765
 Thr Gly Ala Leu Leu Ser Thr Val His Gly Phe Thr Thr Phe Leu Ser
 770 775 780
 Asn Pro Phe Gly Ala Leu Ala Val Gly Leu Leu Val Leu Ala Gly Leu
 785 790 795 800
 Val Ala Ala Phe Phe Ala Tyr Arg Tyr Val Leu Lys Leu Lys Thr Ser
 805 810 815
 Pro Met Lys Ala Leu Tyr Pro Leu Thr Thr Lys Gly Leu Lys Gln Leu
 820 825 830
 Pro Glu Gly Met Asp Pro Phe Ala Glu Lys Pro Asn Ala Thr Asp Thr
 835 840 845
 Pro Ile Glu Glu Ile Gly Asp Ser Gln Asn Thr Glu Pro Ser Val Asn
 850 855 860
 Ser Gly Phe Asp Pro Asp Lys Phe Arg Glu Ala Gln Glu Met Ile Lys
 865 870 875 880
 Tyr Met Thr Leu Val Ser Ala Ala Glu Arg Gln Glu Ser Lys Ala Arg
 885 890 895
 Lys Lys Asn Lys Thr Ser Ala Leu Leu Thr Ser Arg Leu Thr Gly Leu
 900 905 910
 Ala Leu Arg Asn Arg Arg Gly Tyr Ser Arg Val Arg Thr Glu Asn Val
 915 920 925
 Thr Gly Val

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930

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<210> SEQ ID NO 98
<211> LENGTH: 2817
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: pVZV-gB nucleic acid sequence

<400> SEQUENCE: 98
aagcttgcca ccatgtcacc ttgcggatac tactcaaaaat ggcggaatcg ggataggccc      60
gaatacaggc ggaatctgcg gtttaggcgg ttcttcagct ccatccaccc taacgccgct      120
gcaggatctg gcttcaatgg gccaggagtg tttatcacta gtgtcacccg cgtgtggctg      180
tgcttcctgt gtattttctc aatgttgtc accgctgtgg tcagtgtgtc acccagctcc      240
ttttacgagt ccctgcaggt ggaacctacc cagtctgagg acatcacacg aagtgcacac      300
ctgggcgacg gggatgagat ccgagaagcc attcataagt ctcaggatgc tgagacaaaa      360
cccactttct acgtctgccc ccctccaacc ggcagtacaa ttgtgagact ggaaccaacc      420
aggacatgtc ccgactatca cctgggaaaag aacttcaccg aaggcatcgc agtggctctac      480
aaggagaaca tcgccgctta caagtttaaa gccacagtgt actacaagga cgtcatcgtg      540
agcactgcat gggccgggtc tagttacact cagatcacca accgctatgc cgatcgagtc      600
cccattctctg tgagcgagat cactgacacc attgataagt tcggaaaatg ctcaagcaaa      660
gtacacctag tccgcaacaa tcacaaggty gaggccttca acgaagacaa aaatcctcag      720
gatatgccac tgatcgcatac taagtataac tccgtgggct ctaaagcctg gcataccaca      780
aatgatacat acatggtggc aggcacaccc gggacttata gcacagggac ttcagtcaac      840
tgtatcattg aggaagtgga ggcgccggagc attttccat acgactcatt tggcctgagc      900
accggggata tcactctacat gagccccttc tttggactgc gcgacggcgc ataccgagag      960
cactccaatt atgccatgga tcggttccat cagtttgaag gatacagaca gagggacctg      1020
gatacacgag ccctgctgga gccagcagca cgaaacttcc tggtcacacc ccacctgact      1080
gtgggctgga attggaagcc taaaagaacc gaggtctgct ccctggtgaa gtggcgggag      1140
gtggaagacg tggtcagaga tgaatatgcc cataacttca ggtttaccat gaaaacactg      1200
agtactacct tcactctcaga gaccaatgag ttcaacctga atcagattca cctgtctcag      1260
tgtgtgaagg aggaagctcg ggcaatcatt aacagaatct acacaactag gtacaattcc      1320
tctcatgtga gaacaggcga cattcagact tacctggcca gggcggggtt cgtggctcgtg      1380
tttcagcccc tgetgagcaa ctccctggct agactgtatc tgcaggagct ggtgagggaa      1440
aacaccaatc acagcccccga gaagcatcct actaggaaca cccgcagtcg gagatcagtc      1500
cctgtggagc tgcgagccaa tcggaccatc accacaacta gttcagtgga attcgtatg      1560
ctgcagttta catacgacca catccaggag catgtgaatg aaatgctggc tagaattagc      1620
tcctcttggg gccagctgca gaaccgcgag cgagcactgt ggagcggcct gttccaatc      1680
aatccctcog ccctggcttc tacaattctg gaccagcggg tgaaggccag aatcctgggg      1740
gatgtcattt ctgtgagtaa ctgccctgag ctgggaagtg ataccgccat cattctgcag      1800
aattcaatgc ggggtgcagg gagcaccaca aggtgttact cccgcccact gatcagcatt      1860
gtctccctga acggatctgg cacagtggaa ggacagctgg gcaactgaaa tgagctgatc      1920
atgagcagag atctgctgga gccatgtgtg gctaaccaca agaggtactt cctgtttgga      1980
caccattatg tctactatga agactacaga tatgtgaggg agatcgccgt ccatgatgtg      2040

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ggcatgatta gcacctacgt ggacctgaac ctgacactgc tgaagatcg cgaattcatg 2100
ccccctgcagg tgtacacccg ggacgagctg cgagataccg gactgctgga ctatagcgaa 2160
atccagagggc gcaatcagat gcaactccctg cggttttacg acatcgataa ggctcgtgcag 2220
tatgatagcg ggactgctat tatgcaggga atggcacagt tctttcaggg actgggaacc 2280
gctggacagg cagtgggaca cgtcgtgctg ggagcaactg gagctctgct gtctaccgtg 2340
catgggttca ctacctttct gagtaaccct ttcggagcac tggcagtcgg actgctgggtg 2400
ctggctggac tggctcgtgc attcctttgca tacagatatg tgctgaaagt gaaaacatcc 2460
cctatgaagg ccctgtaccc actgacaact aagggcctga aacagctgcc tgaagggatg 2520
gaccatttg cagagaaacc caacgccacc gacacaccaa tcgaggaat tggcgattct 2580
cagaacaccg agccctctgt gaatagtggg ttcgaccctg ataagtttag ggaggcccag 2640
gaaatgatca aatacatgac actggtgtca gcagctgagc gacaggaag caaggcacgg 2700
aagaagaaca agactagcgc tctgctgacc tccaggtga caggactggc actgcgaaac 2760
cgacgaggat atagccgggt gagaactgag aatgtcacgg gcgtgtgata actcgag 2817

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<210> SEQ ID NO 99

<211> LENGTH: 1007

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: pVZV-gHgL amino acid sequence

<400> SEQUENCE: 99

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Met Phe Ala Leu Val Leu Ala Val Val Ile Leu Pro Leu Trp Thr Thr
 1             5             10             15
Ala Asn Lys Ser Tyr Val Thr Pro Thr Pro Ala Thr Arg Ser Ile Gly
 20             25             30
His Met Ser Ala Leu Leu Arg Glu Tyr Ser Asp Arg Asn Met Ser Leu
 35             40             45
Lys Leu Glu Ala Phe Tyr Pro Thr Gly Phe Asp Glu Glu Leu Ile Lys
 50             55             60
Ser Leu His Trp Gly Asn Asp Arg Lys His Val Phe Leu Val Ile Val
 65             70             75             80
Lys Val Asn Pro Thr Thr His Glu Gly Asp Val Gly Leu Val Ile Phe
 85             90             95
Pro Lys Tyr Leu Leu Ser Pro Tyr His Phe Lys Ala Glu His Arg Ala
 100            105            110
Pro Phe Pro Ala Gly Arg Phe Gly Phe Leu Ser His Pro Val Thr Pro
 115            120            125
Asp Val Ser Phe Phe Asp Ser Ser Phe Ala Pro Tyr Leu Thr Thr Gln
 130            135            140
His Leu Val Ala Phe Thr Thr Phe Pro Pro Asn Pro Leu Val Trp His
 145            150            155            160
Leu Glu Arg Ala Glu Thr Ala Ala Thr Ala Glu Arg Pro Phe Gly Val
 165            170            175
Ser Leu Leu Pro Ala Arg Pro Thr Val Pro Lys Asn Thr Ile Leu Glu
 180            185            190
His Lys Ala His Phe Ala Thr Trp Asp Ala Leu Ala Arg His Thr Phe
 195            200            205
Phe Ser Ala Glu Ala Ile Ile Thr Asn Ser Thr Leu Arg Ile His Val
 210            215            220

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645				650				655							
Tyr	Val	Leu	Ile	Leu	Pro	Ala	Val	Gln	Gly	His	Ser	Tyr	Val	Ile	Thr
		660						665						670	
Arg	Asn	Lys	Pro	Gln	Arg	Gly	Leu	Val	Tyr	Ser	Leu	Ala	Asp	Val	Asp
		675					680					685			
Val	Tyr	Asn	Pro	Ile	Ser	Val	Val	Tyr	Leu	Ser	Arg	Asp	Thr	Cys	Val
	690					695					700				
Ser	Glu	His	Gly	Val	Ile	Glu	Thr	Val	Ala	Leu	Pro	His	Pro	Asp	Asn
	705				710					715					720
Leu	Lys	Glu	Cys	Leu	Tyr	Cys	Gly	Ser	Val	Phe	Leu	Arg	Tyr	Leu	Thr
			725						730						735
Thr	Gly	Ala	Ile	Met	Asp	Ile	Ile	Ile	Ile	Asp	Ser	Lys	Asp	Thr	Glu
			740						745						750
Arg	Gln	Leu	Ala	Ala	Met	Gly	Asn	Ser	Thr	Ile	Pro	Pro	Phe	Asn	Pro
		755					760							765	
Asp	Met	His	Gly	Asp	Asp	Ser	Lys	Ala	Val	Leu	Leu	Phe	Pro	Asn	Gly
	770					775					780				
Thr	Val	Val	Thr	Leu	Leu	Gly	Phe	Glu	Arg	Arg	Gln	Ala	Ile	Arg	Met
	785				790					795					800
Ser	Gly	Gln	Tyr	Leu	Gly	Ala	Ser	Leu	Gly	Gly	Ala	Phe	Leu	Ala	Val
			805						810						815
Val	Gly	Phe	Gly	Ile	Ile	Gly	Trp	Met	Leu	Cys	Gly	Asn	Ser	Arg	Leu
		820						825					830		
Arg	Glu	Tyr	Asn	Lys	Ile	Pro	Leu	Thr	Arg	Gly	Arg	Lys	Arg	Arg	Ser
		835					840						845		
Met	Ala	Ser	His	Lys	Trp	Leu	Leu	Gln	Ile	Val	Phe	Leu	Lys	Thr	Ile
	850					855					860				
Thr	Ile	Ala	Tyr	Cys	Leu	His	Leu	Gln	Asp	Asp	Thr	Pro	Leu	Phe	Phe
	865				870					875					880
Gly	Ala	Lys	Pro	Leu	Ser	Asp	Val	Ser	Leu	Ile	Ile	Thr	Glu	Pro	Cys
			885						890						895
Val	Ser	Ser	Val	Tyr	Glu	Ala	Trp	Asp	Tyr	Ala	Ala	Pro	Pro	Val	Ser
			900					905					910		
Asn	Leu	Ser	Glu	Ala	Leu	Ser	Gly	Ile	Val	Val	Lys	Thr	Lys	Cys	Pro
		915					920						925		
Val	Pro	Glu	Val	Ile	Leu	Trp	Phe	Lys	Asp	Lys	Gln	Met	Ala	Tyr	Trp
	930					935					940				
Thr	Asn	Pro	Tyr	Val	Thr	Leu	Lys	Gly	Leu	Ala	Gln	Ser	Val	Gly	Glu
	945				950					955					960
Glu	His	Lys	Ser	Gly	Asp	Ile	Arg	Asp	Ala	Leu	Leu	Asp	Ala	Leu	Ser
			965						970						975
Gly	Val	Trp	Val	Asp	Ser	Thr	Pro	Ser	Ser	Thr	Asn	Ile	Pro	Glu	Asn
			980					985					990		
Gly	Cys	Val	Trp	Gly	Ala	Asp	Arg	Leu	Phe	Gln	Arg	Val	Cys	Gln	
		995					1000						1005		

<210> SEQ ID NO 100

<211> LENGTH: 3045

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: pVZV-gHgL nucleic acid sequence

<400> SEQUENCE: 100

aagcttgcca ccattgttcgc actggtcctg gccgtcgtca tcctgccctt gtggacaact

60

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gctaacaat	cttacgtoac	tctacccct	gcaactcgg	ctatcggcca	catgagtgc	120
ctgctgaggg	aatactcaga	tcgcaacatg	agcctgaaac	tggaggcttt	ctatcccacc	180
ggatttgatg	aggaactgat	taagtctctg	cactggggca	acgaccggaa	gcatgtgttc	240
ctggtcacog	tcaaagtga	tctaccaca	cacgaagggg	acgtcggact	ggcatcttt	300
ccaaaatacc	tgctgagccc	ctatcacttc	aaggcagagc	atcgggcccc	atttcccget	360
ggcagattcg	ggtttctgag	ccatccagtc	acccccgacg	tgctcttctt	tgatagetcc	420
ttcgtccct	acctgactac	ccagcacctg	gtggcattca	caacttttcc	ccctaaccct	480
ctgggtgtgg	atctggagag	ggcagaaact	gcagctaccg	ctgagcgacc	attcggcgtg	540
agcctgctgc	ctgcaaggcc	aacagtcccc	aagaacacta	tccctggaaca	caaagctcat	600
tttgcaactt	gggatgcact	ggccccccac	accttctttt	ctgctgaggg	aatcattaca	660
aatagtactc	tgcgattca	tgtcccctg	ttcgggagtg	tgtggcctat	ccgatactgg	720
gccactggct	cagtgtctgt	gacctctgac	agtgggaggg	tcgaagtga	tattggagtg	780
ggctttatgt	ctagtctgat	cagcctgtca	agcggcctgc	caatcgagct	gattgtggtc	840
ccccacacag	tcaagctgaa	cgccgtgact	tccgatacca	catggttcca	gctgaatcca	900
ccaggacctg	accaggacc	atcttaccga	gtgtatctgc	tggggcgagg	actggacatg	960
aactttagta	agcacgcaac	cgtggatata	tgccctacc	ccgaggaate	actggactac	1020
agatatcacc	tgagcatggc	acatacagag	gccctgagga	tgactaccaa	agccgaccag	1080
cacgatatac	acgaggaate	ttactaccat	atcgcagcca	ggattgctac	ctccatcttc	1140
gcactgtctg	agatgggccc	cacaactgaa	tattttctgc	tggacgagat	cgctgatgtg	1200
cagtaccagc	tgaagtctct	gaactatatt	ctgatgcgaa	tcggagcagg	agctcaacca	1260
aatacaat	ttcaggaactag	cgacctgac	tttgccgac	cttcacagct	gcatgatgaa	1320
ctgagcctgc	tgttcggcca	ggcacaaccc	gcaaacgtgg	actactttat	ctcatatgac	1380
gaggccccgag	atcagctgaa	gaccgcatac	gcaactgagcc	ggggccagga	ccaogtgaat	1440
gctctgtccc	tggcacggag	agtcacatg	tctatctaca	aggggctgct	ggtgaaacag	1500
aacctgaatg	ccacagagcg	gcaggccctg	ttctttgcta	gcatgatcct	gctgaaacttc	1560
agagagggac	tggaaaacag	cagccgggtg	ctggatggac	gaaccacact	gctgctgatg	1620
acctctatgt	gcacagctgc	acacgctact	caggccgctc	tgaacatcca	ggaggggctg	1680
gcatactga	atcctagcaa	gcatatggtt	acaattccca	acgtgtatag	tccttgtatg	1740
ggatcactga	ggaccgacct	gacagaggaa	attcacgtga	tgaacctgct	gagtgccatc	1800
cctaccgcc	caggcctgaa	tgaggtgctg	catacacagc	tggacgagag	cgaattttc	1860
gatgcagcct	ttaaaacaat	gatgatcttc	actacctgga	ctgccaagga	tctgcacatc	1920
ctgcacacc	atgtcccaga	agtgtttaca	tgccaggacg	ctgcagcccc	gaatggcgag	1980
tacgtcctga	ttctgccagc	cgtgcagggg	cattcctatg	tcatcaccag	aaacaagccc	2040
cagaggggccc	tggtgtactc	tctggctgac	gtcgatgtgt	acaatcccat	cagcgtggtc	2100
tatctgtcca	gagatacttg	tgtgagcgag	cacggggcca	ttgaaacctg	ggccctgcct	2160
catccagaca	acctgaaaga	atgcctgtac	tgtgggtccg	tgctcctgcg	gtatctgaca	2220
actggagcta	tcattggat	cattatcatt	gacagcaagg	atacagagag	acagctggct	2280
gcaatgggga	actccactat	tcctcccttc	aaccctgaca	tgcacggaga	cgatagcaaa	2340
gccgtgctgc	tgttcccaaa	tgggactgtg	gtcacccctgc	tgggatttga	aaggcccgag	2400

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gccatcagga tgtccgggca gtacctggga gcttctctgg gaggagcctt cctggctgtg 2460
gtcggatttg gcatcattgg atggatgctg tgcggcaact ccagactgag ggagtataat 2520
aagatcccc tgaccgcgg acgaaaacga cggtcctgg cctctcacia gtggctgtg 2580
cagattgtgt tcctgaaaac catcacaatt gcttactgcc tgcactgtga ggacgatacc 2640
cctctgttct ttggcgcaaa gccactgagt gatgtgtcac tgatcattac agaaccttgt 2700
gtcagttcag tgtacgaggc atgggactat gccgctcccc ctgtgagcaa cctgtccgaa 2760
gccctgtccg gcattgtggt caagacaaa tgtcccgccc ctgaagtgat cctgtggttc 2820
aaggataaac agatggccta ctggaccaat ccatatgtga cactgaaagg gctggctcag 2880
agtgtcggag aggaacacaa gtcaggcgac atcagagatg cactgctgga cgcctgtct 2940
ggcgtctggg tggatagtag ctctagctcc accaacattc cagagaatgg atgcgtgtgg 3000
ggagcagacc gactgttcca gagagtgtgt cagtgataac tcgag 3045

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<210> SEQ ID NO 101

<211> LENGTH: 529

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: pVZV-gMgN amino acid sequence

<400> SEQUENCE: 101

```

Met Gly Thr Gln Lys Lys Gly Pro Arg Ser Glu Lys Val Ser Pro Tyr
1           5           10           15
Asp Thr Thr Thr Pro Glu Val Glu Ala Leu Asp His Gln Met Asp Thr
20           25           30
Leu Asn Trp Arg Ile Trp Ile Ile Gln Val Met Met Phe Thr Leu Gly
35           40           45
Ala Val Met Leu Leu Ala Thr Leu Ile Ala Ala Ser Ser Glu Tyr Thr
50           55           60
Gly Ile Pro Cys Phe Tyr Ala Ala Val Val Asp Tyr Glu Leu Phe Asn
65           70           75           80
Ala Thr Leu Asp Gly Gly Val Trp Ser Gly Asn Arg Gly Gly Tyr Ser
85           90           95
Ala Pro Val Leu Phe Leu Glu Pro His Ser Val Val Ala Phe Thr Tyr
100          105          110
Tyr Thr Ala Leu Thr Ala Met Ala Met Ala Val Tyr Thr Leu Ile Thr
115          120          125
Ala Ala Ile Ile His Arg Glu Thr Lys Asn Gln Arg Val Arg Gln Ser
130          135          140
Ser Gly Val Ala Trp Leu Val Val Asp Pro Thr Thr Leu Phe Trp Gly
145          150          155          160
Leu Leu Ser Leu Trp Leu Leu Asn Ala Val Leu Leu Leu Ala Tyr
165          170          175
Lys Gln Ile Gly Val Ala Ala Thr Leu Tyr Leu Gly His Phe Ala Thr
180          185          190
Ser Val Ile Phe Thr Thr Tyr Phe Cys Gly Arg Gly Lys Leu Asp Glu
195          200          205
Thr Asn Ile Lys Ala Val Ala Asn Leu Arg Gln Gln Ser Val Phe Leu
210          215          220
Tyr Arg Leu Ala Gly Pro Thr Arg Ala Val Phe Val Asn Leu Met Ala
225          230          235          240
Ala Leu Met Ala Ile Cys Ile Leu Phe Val Ser Leu Met Leu Glu Leu
245          250          255

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Val Val Ala Asn His Leu His Thr Gly Leu Trp Ser Ser Val Ser Val
 260 265 270

Ala Met Ser Thr Phe Ser Thr Leu Ser Val Val Tyr Leu Ile Val Ser
 275 280 285

Glu Leu Ile Leu Ala His Tyr Ile His Val Leu Ile Gly Pro Ser Leu
 290 295 300

Gly Thr Leu Val Ala Cys Ala Thr Leu Gly Thr Ala Ala His Ser Tyr
 305 310 315 320

Met Asp Arg Leu Tyr Asp Pro Ile Ser Val Gln Ser Pro Arg Leu Ile
 325 330 335

Pro Thr Thr Arg Gly Thr Leu Ala Cys Leu Ala Val Phe Ser Val Val
 340 345 350

Met Leu Leu Leu Arg Leu Met Arg Ala Tyr Val Tyr His Arg Gln Lys
 355 360 365

Arg Ser Arg Phe Tyr Gly Ala Val Arg Arg Val Pro Glu Arg Val Arg
 370 375 380

Gly Tyr Ile Arg Lys Val Lys Pro Ala His Arg Asn Ser Arg Arg Thr
 385 390 395 400

Asn Tyr Pro Ser Gln Gly Tyr Gly Tyr Val Tyr Glu Asn Asp Ser Thr
 405 410 415

Tyr Glu Thr Asp Arg Glu Asp Glu Leu Leu Tyr Glu Arg Ser Asn Ser
 420 425 430

Gly Trp Glu Arg Gly Arg Lys Arg Arg Ser Met Gly Ser Ile Thr Ala
 435 440 445

Ser Phe Ile Leu Ile Thr Met Gln Ile Leu Phe Phe Cys Glu Asp Ser
 450 455 460

Ser Gly Glu Pro Asn Phe Ala Glu Arg Asn Phe Trp His Ala Ser Cys
 465 470 475 480

Ser Ala Arg Gly Val Tyr Ile Asp Gly Ser Met Ile Thr Thr Leu Phe
 485 490 495

Phe Tyr Ala Ser Leu Leu Gly Val Cys Val Ala Leu Ile Ser Leu Ala
 500 505 510

Tyr His Ala Cys Phe Arg Leu Phe Thr Arg Ser Val Leu Arg Ser Thr
 515 520 525

Trp

<210> SEQ ID NO 102
 <211> LENGTH: 1611
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: pVZV-gMgN nucleic acid sequence

<400> SEQUENCE: 102

aagcttgcca ccatgggac acagaagaag ggaccccgga gcgagaaagt ctcaccatac 60
 gacacaacaa cccccgaggt ggaggcactg gatcatcaga tggacactct gaactggagg 120
 atttggatca ttcaggtcat gatgttcaca ctgggagctg tcatgctgct ggcaactctg 180
 atcgccgcta gctccgaata caccggcatt cctgcttct atgcagcgt ggtcgactac 240
 gagctgttta acgctacact ggatggagga gtgtggtccg gaaatcgagg aggatattct 300
 gccccagtgc tgttcctgga accccacagc gtggtgcct tcacctacta taccgcctg 360
 acagccatgg ctatggcagt gtacactctg atcaccgctg caatcattca tcgggagacc 420
 aagaaccaga gagtgaggca gtctagtgga gtcgcatggc tgggtgctga cccaaccaca 480

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ctgttctggg ggctgctgag cctgtggctg ctgaatgctg tggctctgct gctggcatat 540
aacagatcg gagtggccgc tactctgtac ctgggccact ttgccacctc tgtgattttc 600
actacctatt tttgcgggag aggaaagctg gatgaaacaa acatcaaagc cgtggctaata 660
ctgaggcagc agagcgtctt cctgtaccga ctggcaggac caactcgggc tgtgtttgtc 720
aacctgatgg cagccctgat ggccatctgt attctgttcg tgagcctgat gctggaactg 780
gtggtcgcga atcacctgca taccggcctg tggtaaacgc tgcctcgcgc catgtctacc 840
ttcagcactc tgtcagtggt ctatctgacg gtgagtgagc tgattctggc ccaactacatc 900
catgtgctga ttggacctc actgggaacc ctggctcgcg gcgcaacctt gggaacagct 960
gcacactcct atatggacag actgtacgat cctatcagcg tgcagtcctc cagactgatt 1020
cctacaacta gggggacact ggcttctctg gcagtgttct ctgtggctcat gctgctgctg 1080
cgactgatgc gggcttaoct gtatcacccg cagaagcgca gtcgatttta tggagcagtg 1140
cggagagtcc ctgagcgggt gagaggatac atccgcaagg tcaaacctgc ccatcgaaac 1200
agtaggcgca ccaattatcc atcacaggc tacggctatg tgtacgaaaa cgatagcact 1260
tatgagaccg acagagagga tgaactgctg tacgaaagga gtaattcagg gtgggagagg 1320
ggacgcaaac gacggtctat ggggagtatc acagcttctc tcctcctgat tactatgcag 1380
attctgttct tttgcgagga ctctctgga gaacaaaact tcgccgagcg caatttttgg 1440
cacgcaagct gttccgccag aggcgtgat atcgatggga gcatgattac cacactgttc 1500
ttttacgct ccctgctggg agtgtgcgct gctctgatct ctctggccta ccatgcttgt 1560
ttcagactgt ttaccagatc agtctgcgct agcacatggt gataactcga g 1611

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<210> SEQ ID NO 103

<211> LENGTH: 892

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: pCeHV1-gB amino acid sequence

<400> SEQUENCE: 103

```

Met Arg Pro Arg Ala Gly Pro Leu Pro Leu Pro Ser Pro Leu Val Pro
 1          5          10          15
Leu Leu Ala Leu Ala Leu Leu Ala Ala Thr Arg Pro Leu Gly Pro Ala
 20          25          30
Ala Ala Thr Pro Val Val Ser Pro Arg Ala Ser Pro Ala Pro Pro Val
 35          40          45
Pro Ala Ala Thr Pro Thr Phe Pro Asp Asp Asp Asn Asp Gly Glu Ala
 50          55          60
Gly Ala Ala Pro Gly Ala Pro Gly Thr Asn Ala Ser Val Glu Ala Gly
 65          70          75          80
His Ala Thr Leu Arg Glu Asn Leu Arg Asp Ile Lys Ala Leu Asp Gly
 85          90          95
Asp Ala Thr Phe Tyr Val Cys Pro Pro Pro Thr Gly Ala Thr Val Val
 100         105         110
Gln Phe Glu Gln Pro Arg Pro Cys Pro Arg Ala Pro Asp Gly Gln Asn
 115         120         125
Tyr Thr Glu Gly Ile Ala Val Ile Phe Lys Glu Asn Ile Ala Pro Tyr
 130         135         140
Lys Phe Lys Ala Thr Met Tyr Tyr Lys Asp Val Thr Val Ser Gln Val
 145         150         155         160

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580					585					590					
Tyr	Glu	Glu	Gly	Gly	Pro	Leu	Val	Glu	Gly	Gln	Leu	Gly	Glu	Asp	Asn
	595						600					605			
Glu	Ile	Arg	Leu	Glu	Arg	Asp	Ala	Leu	Glu	Pro	Cys	Thr	Val	Gly	His
610						615					620				
Arg	Arg	Tyr	Phe	Thr	Phe	Gly	Ala	Gly	Tyr	Val	Tyr	Phe	Glu	Asp	Tyr
625					630					635					640
Ala	Tyr	Ser	His	Gln	Leu	Gly	Arg	Ala	Asp	Val	Thr	Thr	Val	Ser	Thr
				645					650					655	
Phe	Ile	Asn	Leu	Asn	Leu	Thr	Met	Leu	Glu	Asp	His	Glu	Phe	Val	Pro
		660						665					670		
Leu	Glu	Val	Tyr	Thr	Arg	Gln	Glu	Ile	Lys	Asp	Ser	Gly	Leu	Leu	Asp
	675						680					685			
Tyr	Thr	Glu	Val	Gln	Arg	Arg	Asn	Gln	Leu	His	Ala	Leu	Arg	Phe	Ala
690						695					700				
Asp	Ile	Asp	Thr	Val	Ile	Lys	Ala	Asp	Ala	His	Ala	Ala	Leu	Phe	Ala
705					710					715					720
Gly	Leu	Tyr	Ser	Phe	Phe	Glu	Gly	Leu	Gly	Asp	Val	Gly	Arg	Ala	Val
				725					730					735	
Gly	Lys	Val	Val	Met	Gly	Ile	Val	Gly	Gly	Val	Val	Ser	Ala	Val	Ser
		740						745					750		
Gly	Val	Ser	Ser	Phe	Leu	Ser	Asn	Pro	Phe	Gly	Ala	Leu	Ala	Val	Gly
		755					760					765			
Leu	Leu	Val	Leu	Ala	Gly	Leu	Ala	Ala	Ala	Phe	Phe	Ala	Phe	Arg	Tyr
770						775					780				
Val	Met	Arg	Leu	Gln	Arg	Asn	Pro	Met	Lys	Ala	Leu	Tyr	Pro	Leu	Thr
785					790					795					800
Thr	Lys	Glu	Leu	Lys	Ser	Asp	Gly	Pro	Ser	Pro	Ala	Gly	Asp	Gly	Gly
				805					810					815	
Asp	Gly	Ala	Ser	Gly	Gly	Gly	Glu	Glu	Asp	Phe	Asp	Glu	Ala	Lys	Leu
		820						825				830			
Ala	Gln	Ala	Arg	Glu	Met	Ile	Arg	Tyr	Met	Ala	Leu	Val	Ser	Ala	Met
		835					840					845			
Glu	Arg	Thr	Glu	His	Lys	Ala	Arg	Lys	Lys	Gly	Thr	Ser	Ala	Leu	Leu
850						855					860				
Ser	Ala	Lys	Val	Thr	Asn	Met	Val	Met	Arg	Lys	Arg	Ala	Lys	Pro	Arg
865					870					875					880
Tyr	Ser	Pro	Leu	Gly	Asp	Thr	Asp	Glu	Glu	Leu					
				885					890						

<210> SEQ ID NO 104
 <211> LENGTH: 2679
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: pCeHV1-gB nucleic acid sequence
 <400> SEQUENCE: 104

```

atgagacctc ggcgggacc cctgccctg ccttcacccc tggtgccct gctggcctg      60
gctctgctgg ctgcaaccg acccctgggc cctgccgctg caaccccagt ggtctcacc      120
agagcaagcc ctgccctcc cgtgccagca gctacaccta ctttccaga cgatgacaac      180
gatggagagg caggagcagc accaggagct cctggcacia acgcatccgt ggaggctggc      240
cacgcaactc tgagggaaaa tctgcgagc atcaaggccc tggacggaga tgctacattc      300
    
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tacgtgtgcc cccccctac aggagcaact gtggtccagt ttgagcagcc tcgaccatgt	360
ccccgggctc cagatggaca gaactacacc gagggcatcg cagtgattht caaggaaaac	420
atcgcacctt acaagtttaa agccacaatg tactacaaag acgtgactgt ctccaagtg	480
tggttcggcc acccgtactc tcagttcatg gggatthttg aggatagagc ccctgtgcca	540
tttgaggaag tcatcgacaa gattaatgca agaggcgtct gcaggagcac cgccaaatat	600
gtgaggaaca atatggagag cacagctttc catcgcatg acgatgaatc cgatatgaag	660
ctgaaaccag caaaggctgc aaccgaaca tcacgggggt ggcacaccac agacctgaaa	720
tacaacccca gccgaatcga gcccttccat cggatggaa ctaccgtgaa ttgtattgtg	780
gaggaagtgc agggccggag cgtgtacca tatgatgaat ttgtcctggc tacaggcgac	840
ttcgtgtaca tgtcaccctt ttacggctat cgcgacgggg ctacgcaga gcatactgcc	900
tatgccgctg acaggttccg ccagggtgat ggatactatg aacgggacct gtctactggc	960
cggagagcaa gtaccctgc cacaagaaac ctgctgacaa ctccaaagt taccgtggga	1020
tgggatggg ccccaaagag gccctccgtc tgcactctga ccaaaggca ggaagtggac	1080
gaaatgctga gggcagagta cggcccaagt ttccgcttta gctcctctgc cctgtcaacc	1140
acattcacta ccaatcggac cgaatatgcc ctgtctagag tggacctggg agattgcgtg	1200
ggcagagagg ccagggaagc tgtggatcgc atcttctga ggcctacaa cgggactcac	1260
gtgaaagtgc gacagggtca gtactatctg gctaccggcg ggtttctgat tgcataccag	1320
cctctgctgt ctaatgcctt ggtggagctg tatgtccgag aactgctgcg agagcaggaa	1380
cgacggccag gcgacgcagc agctacacca aagcctagtg ctgaccacc cgatgtcgag	1440
aggatcaaaa caactagtct agtggaatc gccgcctgc agtttaccta tgatcacatt	1500
cagcggcatg tgaacgacat gctggggaga atcgccattg cttgggtcga gctgcagaac	1560
catgaaactg ccctgtggaa tgaggccagg aagctgaacc ccaatgcaat cgctcagct	1620
acagtgggcc ggcgggtgag cgcgccaatg ctgggagatg tgatggcagt ctccaactgc	1680
gtgcctgtca cccagacaa cgtcattatg cagaattcta tgcgggtgcc cgcagacct	1740
ggcacctgtt acagcagacc cctggtgtcc ttcaggatg aggaaggcgg ccctctggtg	1800
gagggacagc tgggagagga taacgaaatc cgcctggagc gagacgctct ggaaccctgt	1860
actgtgggcc acccgcgata cttcaccttt ggagccggct acgtgtatth tgaggattac	1920
gcctattctc atcagctggg gcgggctgac gtgaccacag tcagtacct catcaacctg	1980
aatctgacaa tgctggagga tcacgaatth gtgcctctgg aggtctacac acggcaggaa	2040
attaaggaca gcgggctgct ggattatact gaggtgcagc ggagaaatca gctgcacgct	2100
ctgagattcg cagacatcga taccgtgatt aaggcagatg cccatgcagc cctgthtgcc	2160
ggactgtaca gctctthtga aggactggga gacgtgggac gagctgtcgg aaaagtggtc	2220
atgggcatcg tgggcccgtt ggtgagcgc gtgagcgggg tcagctcctt cctgagcaac	2280
cctthtggcg ctctggcagt gggactgctg gtccctggcag gactggtgc agcctcttht	2340
gccttcagat acgtgatgcg gctgcagaga aatccaatga aggcctgta tcccctgact	2400
accaaggagc tgaatccga cggaccatct ccagcaggcg acggcgggga tggagctagc	2460
ggaggcgggg aggaagactt tgatgaggct aaactggccc aggctaggga aatgattcgc	2520
tacatggccc tgggtgccc tatggagcgc acagaacaca aggcgccgaaa gaaaggcact	2580
agtgcactgc tgtcagccaa agtgaccaac atggtcatga gaaagagagc caagccacga	2640
tattcaccac tgggcgatc cgacgaagag gaactgtga	2679

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<210> SEQ ID NO 105
 <211> LENGTH: 1088
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: pCeHV1-gHgL amino acid sequence

<400> SEQUENCE: 105

```

Met Ser Ala Arg Arg Arg Asp Arg Ser Thr Gly Met Pro Val Cys Trp
1          5          10          15

Ile Leu Ala Gly Leu Ala Ile Ala Ala Gly Ser Ala Ala Val Pro Ala
20          25          30

Pro Met Arg Ala Leu Glu Arg Glu His Tyr Trp Val Ala Gln Ala Asp
35          40          45

Ser Trp Tyr Arg Asp His Pro Arg Met Arg Ala Tyr Trp Arg Asp Gly
50          55          60

Glu Pro Ser Arg Leu Trp Leu Pro Asn Leu Pro Asn Ala Thr Lys Leu
65          70          75          80

Pro Leu Gly Leu Leu Ala Pro Pro Ala Glu Leu Asn Leu Thr Val Ala
85          90          95

Thr Ala Pro Leu Leu Arg Trp Ala Thr Pro Arg Ser Cys Phe Leu Phe
100         105         110

Ile Thr Thr Pro Glu Phe Pro Arg Asn Pro Gly Gln Leu Leu Tyr Val
115         120         125

Asn Lys Thr Ala Leu Leu Gly Leu Pro Ala Asn Ala Ser Leu Pro Ala
130         135         140

Ala Ala Pro Thr Pro Arg Ala Pro Gln Leu Val Ala Gln Leu Arg Gly
145         150         155         160

Phe Leu Gly Asn Pro Ser Ala Ala Ala Leu Leu Arg Ser Arg Ala Trp
165         170         175

Val Thr His Ala Pro Val Trp Asn Pro Arg Ser Leu Val Arg Pro Pro
180         185         190

Val Asp Pro Ser Gly Asp Ile Ala Pro Thr His Ala Pro Arg Pro Pro
195         200         205

Ala Gly Phe Pro Pro Asp Ala Gly Pro Ala Asp Ala Asp Pro Arg Ile
210         215         220

Ser Phe Arg Glu Leu Ser Ala Ala His Leu Asn Asn Ala Ser Gly Thr
225         230         235         240

Trp Leu Val Ala Ala Gly Leu Leu Arg Ala Pro Ser Ala Leu Val Tyr
245         250         255

Arg Ser Pro Ser Ser Ala Thr Trp Pro Leu Ala Ile Trp Ala Thr Gly
260         265         270

Glu Leu Ala Phe Gly Cys Asp Ala Ala Leu Val Arg Ala Arg Tyr Gly
275         280         285

Leu Arg Phe Met Gly Leu Ser Leu Ser Met Arg Asp Ser Ala Pro Ala
290         295         300

Glu Val Leu Val Val Pro Ala Ala Glu Thr Leu Ala Leu Ile Gly Pro
305         310         315         320

Pro Ala Met Asn Glu Pro Leu Val Leu Pro Gly Pro Pro Pro Gly Lys
325         330         335

Arg Tyr Arg Thr Phe Val Ile Gly Ser Val Val Asp Pro Arg Asn Val
340         345         350

Ser Ala Ile Glu Ala Leu Arg Arg Ala Ala Arg Tyr Pro His Glu Asp
355         360         365
  
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Ala Gly His Glu His His Leu Ser Arg Ala Tyr Ala Glu Ile Phe Gly
370 375 380

Glu Gly Pro Ser Val Glu Pro Gly Pro Arg Pro Pro Leu Phe Trp Arg
385 390 395 400

Val Ser Ala Leu Leu Ala Thr Ser Gly Phe Ala Phe Thr Glu Thr Thr
405 410 415

Arg Ala Arg Gly Met Leu Arg Leu Ser Asp Leu Val Asp Phe Leu Ala
420 425 430

His Val Arg Val Ile Ala Asn Leu Ala Leu Arg Gly Ala Ala Gly Cys
435 440 445

Ala Pro Gly Thr Pro Phe Ala Arg Ala Pro Leu Trp Ala Ala Pro Ala
450 455 460

Arg Ala Glu Leu Glu Ser Arg Leu Gly Arg Leu Ala Ala Glu Ala Val
465 470 475 480

Ala Arg Asp Gln Arg Leu Ser Ala Leu Ala Val Ala Tyr Gln Val Ala
485 490 495

Phe Ala Leu Gly Asp Pro Ala Ile Ala Glu Ala Val Ala Pro Ser Ala
500 505 510

Ala His Thr Leu Asp Thr Leu Tyr Ala Glu Phe Leu Arg Gly Arg Gly
515 520 525

Leu Asp Ala Pro Ala Val Arg Arg Ala Leu Phe Tyr Ala Thr Ala Val
530 535 540

Leu Arg Ala Pro Ala Glu Arg Gly Gly Ala Pro Ser Asp Ala Gln Val
545 550 555 560

Thr Arg Gly Arg Arg Ser Leu Leu Leu Ala Ser Ala Met Cys Thr Ser
565 570 575

Asp Val Ala Val Ala Thr His Thr Asp Leu Arg Asp Ala Leu Asp Arg
580 585 590

Ser Asp His Arg Lys Thr Phe Phe Tyr Ala Pro Asp His Phe Ser Pro
595 600 605

Cys Ala Ala Ser Leu Arg Phe Asp Leu Ala Glu Arg Ser Phe Val Met
610 615 620

Asp Thr Leu Ala His Thr Pro Arg Ser Asn Val Ser Val Glu Ala Met
625 630 635 640

Ala Gln Lys Thr Gln Gly Val Ala Ser Ala Leu Thr Arg Trp Ala His
645 650 655

Ala Asn Ala Leu Ile Arg Ala Phe Val Pro Glu Ala Ala Gln Thr Cys
660 665 670

Ala Gly Pro Thr His Asn Ala Glu Pro Leu Val Val Leu Pro Val Thr
675 680 685

Trp Asn Ala Ser Tyr Val Val Thr His Ala Pro Leu Pro Arg Gly Val
690 695 700

Gly Tyr Arg Leu Ala Gly Val Asp Val Arg Arg Pro Leu Phe Leu Thr
705 710 715 720

Tyr Leu Thr Glu Thr Cys Glu Gly Arg Thr Arg Glu Ile Glu Pro Lys
725 730 735

Arg Leu Thr Arg Thr Glu Thr Arg Arg Asp Leu Gly Leu Val Gly Ala
740 745 750

Val Phe Met Arg Tyr Thr Pro Ala Gly Glu Ile Met Ser Ala Leu Val
755 760 765

Val Asp Ser Asp His Thr Gln Gln Gln Leu Ala Gly Gly Pro Leu Ala
770 775 780

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Gly Gly Val Asp Val Phe Val Ser Asp Val Pro Ser Thr Ala Leu Leu
 785 790 795 800
 Leu Phe Pro Asn Gly Thr Val Ile His Leu Leu Ala Phe Asp Thr Leu
 805 810 815
 Pro Leu Ala Thr Ile Thr Pro Gly Val Leu Ala Ala Ser Val Leu Gly
 820 825 830
 Val Val Leu Ile Ala Ala Ala Ile Val Gly Leu Ala Arg Val Ala Trp
 835 840 845
 Thr Cys Val Pro Ser Leu Trp Ser Arg Glu Arg Gly Arg Lys Arg Arg
 850 855 860
 Ser Phe Leu Arg Ser Val Ser Ala Ala Pro Ser Val Val Ser Pro Ala
 865 870 875 880
 Ala Ser Pro Ser Pro Ser Pro Pro Val Glu Tyr Val Ile Arg Ser Val
 885 890 895
 Ala Ala Arg Thr Val Gly Asp Ile Leu Lys Phe Ala Cys Leu Glu Leu
 900 905 910
 Pro Ala Gly Gly Val Thr Trp Arg Tyr Glu Ala Pro Arg Ser Ile Asp
 915 920 925
 Tyr Ala Arg Ile Asp Gly Ile Phe Leu Arg Tyr His Cys Pro Gly Leu
 930 935 940
 Asp Thr Val Val Trp Asp Gly Lys Ala Gln Arg Ala Tyr Trp Val Asn
 945 950 955 960
 Pro Phe Leu Phe Ala Ala Gly Phe Leu Glu Asp Leu Gly His Ala Leu
 965 970 975
 Phe Pro Ala Asn Ala Leu Glu Thr Thr Thr Arg Phe Ala Leu Tyr Lys
 980 985 990
 Glu Val Arg Leu Ala Leu Ala Ser Arg Ser Asp Ala Ala Ser Ser Thr
 995 1000 1005
 Pro Val Pro Pro Gly Cys Val Asp Ala Glu Tyr Ser Arg Thr Arg
 1010 1015 1020
 Asp Cys Pro Asp Gly Arg Thr Pro Gly Ile Trp Asn Glu Pro Arg
 1025 1030 1035
 Ile Arg Arg Pro Phe Ser Ala Pro Asn Asp Glu Ala Ser Pro Gln
 1040 1045 1050
 Pro Gln Ser Leu Ala Pro Ala Pro Thr Pro Thr Pro Pro Gly Arg
 1055 1060 1065
 Thr His Glu Pro Ala Arg Lys Pro Arg Gly Asn Ala Thr Arg Thr
 1070 1075 1080
 Ala Arg Pro Arg Ala
 1085

<210> SEQ ID NO 106
 <211> LENGTH: 3267
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: pCeHV1-gHgL nucleic acid sequence

<400> SEQUENCE: 106

atgtccgcaa gaagacggga ccgaagcact ggaatgcctg tctgttgat cctggctgga 60
 ctggctatcg ctgccgggag cgccgcagtg cccgctccta tgcgagcact ggagcgggaa 120
 cactactggg tggtccagc agactcctgg tatecggatc atccacgaat gcgagcatac 180
 tggagggagc gagagccttc tcgcctgtgg ctgcccaacc tgcctaatac cacaaagctg 240
 ccactgggac tgctggcccc tcccgctgaa ctgaacctga ccgtggcaac agctccctg 300

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ctgagatggg caaccctcg cagctgcttc ctgtttatca ccacaccaga gtttccccgg	360
aaccttgggc agctgctgta tgtgaacaag accgacctgc tgggactgcc agcaaatgcc	420
agcctgcctg cagctgcacc aacccccaga gccctcagc tggctgcccc gctgcgagga	480
ttcctgggaa acccatcgcg cgtgcactg ctgagatcta gggcctgggt cacacacgct	540
cccgtgtgga atccaagaag cctggtcagg ccacctgtgg acccttccgg cgatatcgca	600
ccaactcatg ctctctgccc tccagcagga ttcctcccc atgctggacc agctgacgca	660
gatcctcgca tttcttttcg agagctgtct gccctcacc tgaacaatgc cagcggaaac	720
tggctggtcg ccgcaggact gctgcgagca ccaagcggc tggctctatc gtccccaaac	780
tccgccaat ggccactggc tatctgggca actggcgagc tggccttcgg gtgtgacgct	840
gcaactgtgc gcgcacgata cggactgcgg ttcattggcc tgctactgag catgagggat	900
agcgcctcag ctgaggtgct ggtcgtgcca gccgctgaaa cactggcact gattgggcca	960
cccgcctga acgagccact ggtgctgcca ggacctccac ccggcaagcg gtacagaacc	1020
tttgtgatcg gaagtgtggt cgaccccaga aatgtctcag ccattgaage tctgctggaga	1080
gcagccaggt atcctcagca ggatgcccgc catgaacacc atctgtctag agcatacgcc	1140
gagatcttcg gagaaggacc cagtgtggag cctggaccac gacctccact gttttggcgg	1200
gtgtctgca tctggtggcc tagtggatc gcttttacgc aaactaccag ggcccggcgc	1260
atgctgagggc tgagcgacct ggtggatttc ctggcccacg tgagagtcac tgctaacctg	1320
gcaactgagag gcgcccagc atgcgcacca ggaaccccc ttgctcgcgc accactgtgg	1380
gcagctccag cccgggctga gctggaatca cgactgggccc gactggcagc agaggcagtg	1440
gccccggacc agagactgag cgcctcggca gtcgcctatc aggtggcttt cgcactgggc	1500
gatccagcaa tctgctgagc agtggcacct tccgctgcac aactctgga caccctgat	1560
gccgaattcc tgcgaggacg aggactggat gctccagcag tgaggcgcgc cctgttttac	1620
gccacagctg tcctgcgagc acctgcagag cggggcgggg caccatctga cgccaagtg	1680
actagaggcc gacggagtct gctgctggct tcagcaatgt gcaccagcga tgtggccgtc	1740
gctacacata ctgacctgag ggatgcccctg gaccggagcg atcacagaaa gacctcttt	1800
tacgccccctg accatctttc cccatgtgcc gcttctctga gattcgacct ggccgagagg	1860
tcctttgtga tggatacact ggcccacact cccagaagta acgtgtcagt cgaagcaatg	1920
gcccagaaaa cccagggcgt ggcttctgca ctgacaagat gggcccatgc taatgcaactg	1980
attagggcct tctgtcctga ggcagcacag acctgcctg gaccaacaca caacgccgaa	2040
cccctggtgg tcctgcctgt gacttggaaat gcttctatg tggctaccca tgcccctctg	2100
cctagaggcg tgggatacag gctggcagga gtggacgtgc gggggcccc gttcctgacc	2160
tatctgaccg agacatgtga agggagaaca agggagatcg aacaaaaag gctgactcgc	2220
accgagacac gccgagatct gggcctggtc ggggcctgt ttatgagga cacaccgct	2280
ggggaaatta tgtcagcct ggtggtcgac agcgatcaca ctcagcagca gctggccggc	2340
ggacctctgg ccggggaggt ggacgtgttc gtgagcagtg tgccaagcac cgcctgctg	2400
ctgttcccc atggcacagt gatccatctg ctggcttttg aactctgccc tctggccact	2460
attaccccag gggctcctggc tgcacccgtg ctgggagtg tctgatcgc cgctgcaatt	2520
gtcggactgg cccgctggc ttggacctgc gtcctagcc tgtggctccc cgagcgagga	2580
cgaaagcgga gaagtctct gcggctcgtg tctgcccctc catctgtggt cagtccagca	2640

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gcaagtccat caccaagccc tcccgctgaa tacgtgatcc gctctgtggc tgcacgaact 2700
gtcggagaca ttctgaaatt cgcttgcoctg gagctgcccag ccggcggggg gacctggcgg 2760
tacgaagctc ccagaagcat cgactatgcc agaatcgatg gcatttttct gaggtatcac 2820
tgtccaggac tggacaccgt ggtctgggat gggaaggcac agcgcgccta ctgggtgaac 2880
ccattcctgt ttgccgtgg cttcctggag gatctggggc atgccctgtt tcccgccaat 2940
gctctggaga caactaccg gtttgcoctg tataaagaag tgcgcctggc actggcctcc 3000
cggctgagc cagcctctag taccacagtg ccaccggat gcgtcgatgc agagtacagt 3060
agaacaaggg actgtcctga tgggcgcact ccaggaatct ggaacgagcc ccggattag 3120
cgccctttct cagctccaaa tgacgaagca agtctcagc cacagtcact ggctcccgca 3180
cctacaccaa ctctccagg ccggacccat gaaccgcta ggaaaccaag aggaaatgct 3240
acccgaaccg ccagaccaag agcttga 3267

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<210> SEQ ID NO 107

<211> LENGTH: 867

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: pCeHV1-gCgD amino acid sequence

<400> SEQUENCE: 107

```

Met Ala Gly Trp Arg Ala Ala Gly Ser Gly Leu Cys Leu Phe Val Leu
1           5           10           15
Met Trp Leu Leu Cys Ala Gly Ala Gly Ala Pro Arg Gly Ala Ala Ser
20          25          30
Thr Pro Ala Gly Arg Pro Gly Ala Ser Arg Pro Gly Gly Val Glu Arg
35          40          45
Ala Asn Arg Thr Ala Ala Pro Ala Arg Gly Arg Gly Ser Ser Asn Gly
50          55          60
Thr Gly Pro Gly Ser Thr Ser Ala Gln Phe Arg Cys Lys Arg Pro Asp
65          70          75          80
Val Ser Ala Leu Tyr Gly Ser Arg Val Val Ile Gly Cys Arg Leu Pro
85          90          95
Arg Pro Thr Ala Asp Phe Arg Leu Gln Ile Trp Arg Val Ala Ala Ala
100         105         110
Ala His Thr Glu Pro Val Glu Pro Gly Ala Val Leu Val Asn Val Thr
115         120         125
Ala Pro Pro Asp Gly Glu Leu Val Tyr Asp Ser Ala Pro Asn Arg Thr
130         135         140
Glu Ala Arg Val Arg Trp Ala Glu Gly Ala Gly Pro Asp Ala Arg Pro
145         150         155         160
Arg Val Tyr Ser Ile Glu Gly Thr Phe Pro Thr Gln Arg Leu Val Ile
165         170         175
Gln Glu Leu Thr Val Ala Arg Gln Gly Leu Tyr Leu Trp Ile Arg Gly
180         185         190
Pro Ala Glu Arg Pro Leu Arg Tyr Gly Thr Trp Thr Arg Val Arg Met
195         200         205
Leu Arg Arg Pro Ser Leu Ser Ile Arg Ala His Thr Val Leu Glu Gly
210         215         220
Glu Pro Phe Gly Ala Thr Cys Val Ala Ala Asn Tyr Tyr Pro Gly Asp
225         230         235         240
Arg Ala Ala Phe Arg Trp Phe Glu Gly Gly Gly Glu Val Val Ala Pro
245         250         255

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Glu Arg Val Gln Thr Arg Val Asp Ala Gln Arg Asn Gly Phe Ser Ala
 260 265 270
 Thr Ser Thr Leu Thr Ser Glu Ala Arg Ala Gly Leu Ala Pro Pro Arg
 275 280 285
 Asn Leu Thr Cys Glu Phe Thr Trp His Arg Asp Ser Val Ser Phe Ser
 290 295 300
 Arg Arg Asn Ala Thr Gly Ala Pro Thr Val Leu Pro Arg Pro Thr Ile
 305 310 315 320
 Glu Met Glu Phe Gly Ser Gly Glu Ala Val Cys Thr Ala Ala Cys Val
 325 330 335
 Pro Glu Gly Val Glu Leu Gln Trp Leu Leu Gly Ala Asp Pro Ala Pro
 340 345 350
 Ala Glu Asp Ala Ala Ala Ser Gly Gly Pro Cys Pro Gly His Pro Gly
 355 360 365
 Leu Ala Arg Val Arg Ser Ala Leu Pro Leu Ser Arg Glu His Ser Glu
 370 375 380
 Tyr Thr Cys Arg Leu Val Gly Tyr Pro Pro Thr Val Pro Val Leu Glu
 385 390 395 400
 His His Gly Arg His Glu Pro Ala Pro Arg Asp Pro Val Gly Gln Gln
 405 410 415
 Val Thr Thr Ala Leu Glu Trp Ala Gly Ile Ala Ala Gly Ser Ala Ala
 420 425 430
 Ala Ile Gly Leu Ala Val Gly Val Gly Val Tyr Val Arg Arg Ala Val
 435 440 445
 Ala Arg Arg Arg Arg Val Arg Thr Gly Arg Trp Ala Gly Glu Pro Ala
 450 455 460
 Arg Arg Gly Arg Gly Arg Lys Arg Arg Ser Gly Pro Gly Ile Ala Ala
 465 470 475 480
 Val Leu Leu Ser Leu Ala Val Ala Leu Ala Arg Val Pro Ala Gly Gly
 485 490 495
 Gly Glu Tyr Val Pro Val Glu Arg Ser Leu Thr Arg Val Asn Pro Gly
 500 505 510
 Arg Phe Arg Gly Ala His Leu Ala Pro Leu Glu Gln Lys Thr Asp Pro
 515 520 525
 Pro Asp Val Arg Arg Val Tyr His Val Gln Pro Phe Val Glu Asn Pro
 530 535 540
 Phe Gln Thr Pro Ser Val Pro Val Ala Val Tyr Tyr Ala Val Leu Glu
 545 550 555 560
 Arg Ala Cys Arg Ser Val Leu Leu Trp Ala Pro Thr Glu Ala Val Gln
 565 570 575
 Val Val Arg Gly Ala Pro Glu Ala Thr Arg Pro Asp Ala Arg Tyr Asn
 580 585 590
 Leu Thr Val Ala Trp Tyr Arg Thr Ser Asp Asp Cys Ala Ile Pro Ile
 595 600 605
 Leu Val Met Glu Tyr Ala Glu Cys Pro Tyr Asp Arg Pro Leu Gly Ala
 610 615 620
 Cys Pro Val Arg Asn Leu Pro Arg Trp Ser Phe Tyr Asp Asn Phe Ser
 625 630 635 640
 Ala Thr Ser Asp Asp Asp Leu Gly Leu Val Met His Ala Pro Ala Phe
 645 650 655
 Glu Thr Ala Gly Thr Tyr Val Arg Leu Val Lys Val Asn Gly Trp Val
 660 665 670

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Glu	Val	Thr	Gln	Phe	Ile	Phe	Glu	His	Arg	Gly	Lys	Gly	Pro	Cys	Arg
		675					680					685			
Tyr	Thr	Leu	Pro	Leu	Arg	Ile	Leu	Pro	Ala	Ala	Cys	Leu	Arg	Gly	Pro
	690					695					700				
Val	Phe	Glu	Gln	Gly	Val	Thr	Val	Asp	Gly	Ile	Gly	Met	Leu	Pro	Arg
705					710					715					720
Phe	Ile	Pro	Glu	Asn	Gln	Arg	Ile	Val	Ala	Val	Tyr	Ser	Leu	Gln	Ala
				725					730					735	
Ala	Gly	Trp	His	Gly	Pro	Lys	Ala	Pro	Phe	Thr	Ser	Thr	Leu	Leu	Pro
			740					745					750		
Pro	Glu	Val	Val	Glu	Thr	Ala	Asn	Ala	Thr	Arg	Pro	Glu	Leu	Ala	Pro
		755					760					765			
Glu	Asp	Glu	Asp	Glu	Gln	Ala	Pro	Gly	Asp	Glu	Pro	Ala	Pro	Ala	Val
	770					775					780				
Ala	Ala	Gln	Leu	Pro	Pro	Asn	Trp	His	Val	Pro	Glu	Ala	Ser	Asp	Val
785					790					795					800
Thr	Ile	Gln	Gly	Pro	Ala	Pro	Ala	Pro	Ser	Gly	His	Thr	Gly	Ala	Ile
				805					810						815
Val	Gly	Ala	Leu	Ala	Gly	Ala	Gly	Leu	Ala	Ala	Gly	Val	Val	Val	Leu
			820					825					830		
Ala	Val	Tyr	Leu	Val	Arg	Arg	Arg	Ala	Arg	Ala	Ala	Gly	Lys	His	Val
		835					840					845			
Arg	Leu	Pro	Glu	Leu	Leu	Asp	Glu	Gly	Pro	Gly	Pro	Ala	Arg	Arg	Gly
	850					855					860				
Ala	Pro	Tyr													
865															

<210> SEQ ID NO 108

<211> LENGTH: 2604

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: pCeHV1-gCgD nucleic acid sequence

<400> SEQUENCE: 108

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atggctggat gggaggctgc cgggagcggg ctgtgctgt ttgtcctgat gtggctgctg      60
tgcgctggag ctggagcacc cggaggggca gcttctacac cagctgggcg ccttgagca      120
agtcggccag gcggggtgga gcgagctaac cgaactgcag caccagcagc agggcgagga      180
agctccaatg gcacagggcc tggatctact agtgcccagt tccggtgcaa gagaccagac      240
gtgagcgcgc tgtacggatc cagggtggtc atcggatgta ggctgccacg acctaccgca      300
gactttagac tgcagatttg gagggtggct gcagccgctc aactgaacc agtcgagcct      360
ggagccgtcc tgggtgaactg caccgctccc cctgatggag agctgggtgta cgactccgca      420
cccaatcgga ctgaagccag agtgaggtgg gcagagggag ctggaccaga tgcacgaccc      480
cgagtgtatt ctatcgaagg caccttcctt acacagcggc tggatcatcca ggagctgacc      540
gtcgcacgac agggactgta cctgtggatc agagggcctg ctgagcgacc actgcggtat      600
ggcaacttga cccgggtgag aatgctgcgg agaccttcac tgagcattcg agcacacaca      660
gtgctggagg gagaaccctt cggggctact tgcgtggcag ccaactacta tcctggcgat      720
cgggctgcat tcagatggtt tgaggcgggc ggcgaggtgg tcgcaccaga gagggtgcag      780
acccgcgtcg acgcacagag aaatggcttt tcagccacaa gcaactctgac ctccgaagct      840
cgggcaggac tggccccacc cagaaacctg acctgtgagt tcacttggca tcgggatcc      900

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gtgtctttta gtaggcgcaa tgcaaccggc gccctacag tgctgccaag acccacaatc 960
gagatggaat ttggatctgg cgaagccgtg tgcaactgcc cttgctgccc agaaggagtc 1020
gagctgcagt ggctgctggg agcagatcct gcaccagctg aggacgcagc agctagtgga 1080
ggcccatgcc ctggacaccc tggactggcc aggggtgcct cagctctgcc actgagtagg 1140
gaacattcag agtacacttg tcgcctgggtg ggctatectc caaccgtgcc tgtcctggaa 1200
caccatggac gccacgagcc agccccaga gaccagctgg gacagcaggt caccacagca 1260
ctggaatggg caggaatcgc agcaggaagc gccgcagcaa ttggactggc agtgggagtc 1320
ggagtgtacg tccgacgggc agtggcaaga aggcgccgag tcagaacagg gaggtgggct 1380
ggagagccag cacggagagg acgaggacga aagaggcgct caggaccagg cattgctgca 1440
gtgctgctga gcctggctgt ggcactggcc cgggtcccag ccgggggagg cgaatacgtg 1500
ccagtcgagc gaagcctgac ccgggtgaac ccaggcccgt tccggggcgc ccacctggca 1560
cctctggagc agaaaacaga tccccctgac gtgcggcggg tgtaccatgt ccagcccttc 1620
gtgaaaaatc cttttcagac cccatctgtg cccgtcccg tgtaactatgc tgtgctggag 1680
cgagcatgcc gaagtgtcct gctgtgggca ccaaccgaag cagtgcaggt ggtcaggggc 1740
gccccagagg ctacaagacc cgatgctagg tacaacctga ccgtggcatg gtatgcaca 1800
agcgacgatt gtccatccc catcctggtc atggaatacg ctgagtgcc ctatgataga 1860
cctctgggag cctgtcctgt gcgcaacctg ccacgatgga gcttctacga caatttttc 1920
gccacatctg acgatgaact gggcctggtc atgcacgctc ccgcattoga gactgccggg 1980
acctatgtga ggctggtcaa ggtgaacgga tgggtcgaag tgactcagtt catctttgag 2040
catagaggga aaggaccatg caggtacacc ctgccactgc gaattctgcc tgcagcttgt 2100
ctgcgaggac ccgtgttoga acagggagtc accgtggacg gcacccggat gctgccaagg 2160
tttatccccg agaatcagcg cattgtgcc gtgtatagcc tgcaggcagc aggatggcac 2220
ggacctaagg caccctcacc ctccactctg ctgccaccgc aagtggtcga gactgccaac 2280
gctaccaggc ctgaactggc ccagaggat gaagacgagc aggtccagg ggatgagcct 2340
gcaccagcag tggctgcaca gctgcctcca aattggcacg tgccagaggc ctccgacgtg 2400
accatccagg gaccagctcc tgcacatct ggacatacag gagcaattgt gggcgccctg 2460
gctggagcag gactggcagc tgggtgggtc gtgctggcag tgtacctggt cagaaggcgc 2520
gctcgcgcag caggcaaaca tgtgagactg cctgaactgc tggatgaagg acctggacct 2580
gctcggagag gagccccata ctga 2604

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<210> SEQ ID NO 109

<211> LENGTH: 984

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: VZV-gEg1 amino acid sequence

<400> SEQUENCE: 109

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Met Gly Thr Val Asn Lys Pro Val Val Gly Val Leu Met Gly Phe Gly
1           5           10          15

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Ile Ile Thr Gly Thr Leu Arg Ile Thr Asn Pro Val Arg Ala Ser Val
20          25          30

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Leu Arg Tyr Asp Asp Phe His Ile Asp Glu Asp Lys Leu Asp Thr Asn
35          40          45

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Ser Val Tyr Glu Pro Tyr Tyr His Ser Asp His Ala Glu Ser Ser Trp
50          55          60

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Val Asn Arg Gly Glu Ser Ser Arg Lys Ala Tyr Asp His Asn Ser Pro
 65 70 75 80
 Tyr Ile Trp Pro Arg Asn Asp Tyr Asp Gly Phe Leu Glu Asn Ala His
 85 90 95
 Glu His His Gly Val Tyr Asn Gln Gly Arg Gly Ile Asp Ser Gly Glu
 100 105 110
 Arg Leu Met Gln Pro Thr Gln Met Ser Ala Gln Glu Asp Leu Gly Asp
 115 120 125
 Asp Thr Gly Ile His Val Ile Pro Thr Leu Asn Gly Asp Asp Arg His
 130 135 140
 Lys Ile Val Asn Val Asp Gln Arg Gln Tyr Gly Asp Val Phe Lys Gly
 145 150 155 160
 Asp Leu Asn Pro Lys Pro Gln Gly Gln Arg Leu Ile Glu Val Ser Val
 165 170 175
 Glu Glu Asn His Pro Phe Thr Leu Arg Ala Pro Ile Gln Arg Ile Tyr
 180 185 190
 Gly Val Arg Tyr Thr Glu Thr Trp Ser Phe Leu Pro Ser Leu Thr Cys
 195 200 205
 Thr Gly Asp Ala Ala Pro Ala Ile Gln His Ile Cys Leu Lys His Thr
 210 215 220
 Thr Cys Phe Gln Asp Val Val Val Asp Val Asp Cys Ala Glu Asn Thr
 225 230 235 240
 Lys Glu Asp Gln Leu Ala Glu Ile Ser Tyr Arg Phe Gln Gly Lys Lys
 245 250 255
 Glu Ala Asp Gln Pro Trp Ile Val Val Asn Thr Ser Thr Leu Phe Asp
 260 265 270
 Glu Leu Glu Leu Asp Pro Pro Glu Ile Glu Pro Gly Val Leu Lys Val
 275 280 285
 Leu Arg Thr Glu Lys Gln Tyr Leu Gly Val Tyr Ile Trp Asn Met Arg
 290 295 300
 Gly Ser Asp Gly Thr Ser Thr Tyr Ala Thr Phe Leu Val Thr Trp Lys
 305 310 315 320
 Gly Asp Glu Lys Thr Arg Asn Pro Thr Pro Ala Val Thr Pro Gln Pro
 325 330 335
 Arg Gly Ala Glu Phe His Met Trp Asn Tyr His Ser His Val Phe Ser
 340 345 350
 Val Gly Asp Thr Phe Ser Leu Ala Met His Leu Gln Tyr Lys Ile His
 355 360 365
 Glu Ala Pro Phe Asp Leu Leu Leu Glu Trp Leu Tyr Val Pro Ile Asp
 370 375 380
 Pro Thr Cys Gln Pro Met Arg Leu Tyr Ser Thr Cys Leu Tyr His Pro
 385 390 395 400
 Asn Ala Pro Gln Cys Leu Ser His Met Asn Ser Gly Cys Thr Phe Thr
 405 410 415
 Ser Pro His Leu Ala Gln Arg Val Ala Ser Thr Val Tyr Gln Asn Cys
 420 425 430
 Glu His Ala Asp Asn Tyr Thr Ala Tyr Cys Leu Gly Ile Ser His Met
 435 440 445
 Glu Pro Ser Phe Gly Leu Ile Leu His Asp Gly Gly Thr Thr Leu Lys
 450 455 460
 Phe Val Asp Thr Pro Glu Ser Leu Ser Gly Leu Tyr Val Phe Val Val
 465 470 475 480

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Tyr Phe Asn Gly His Val Glu Ala Val Ala Tyr Thr Val Val Ser Thr
 485 490 495
 Val Asp His Phe Val Asn Ala Ile Glu Glu Arg Gly Phe Pro Pro Thr
 500 505 510
 Ala Gly Gln Pro Pro Ala Thr Thr Lys Pro Lys Glu Ile Thr Pro Val
 515 520 525
 Asn Pro Gly Thr Ser Pro Leu Leu Arg Tyr Ala Ala Trp Thr Gly Gly
 530 535 540
 Leu Ala Ala Val Val Leu Leu Cys Leu Val Ile Phe Leu Ile Cys Thr
 545 550 555 560
 Ala Lys Arg Met Arg Val Lys Ala Tyr Arg Val Asp Lys Ser Pro Tyr
 565 570 575
 Asn Gln Ser Met Tyr Tyr Ala Gly Leu Pro Val Asp Asp Phe Glu Asp
 580 585 590
 Ser Glu Ser Thr Asp Thr Glu Glu Glu Phe Gly Asn Ala Ile Gly Gly
 595 600 605
 Ser His Gly Gly Ser Ser Tyr Thr Val Tyr Ile Asp Lys Thr Arg Arg
 610 615 620
 Gly Arg Lys Arg Arg Ser Met Phe Leu Ile Gln Cys Leu Ile Ser Ala
 625 630 635 640
 Val Ile Phe Tyr Ile Gln Val Thr Asn Ala Leu Ile Phe Lys Gly Asp
 645 650 655
 His Val Ser Leu Gln Val Asn Ser Ser Leu Thr Ser Ile Leu Ile Pro
 660 665 670
 Met Gln Asn Asp Asn Tyr Thr Glu Ile Lys Gly Gln Leu Val Phe Ile
 675 680 685
 Gly Glu Gln Leu Pro Thr Gly Thr Asn Tyr Ser Gly Thr Leu Glu Leu
 690 695 700
 Leu Tyr Ala Asp Thr Val Ala Phe Cys Phe Arg Ser Val Gln Val Ile
 705 710 715 720
 Arg Tyr Asp Gly Cys Pro Arg Ile Arg Thr Ser Ala Phe Ile Ser Cys
 725 730 735
 Arg Tyr Lys His Ser Trp His Tyr Gly Asn Ser Thr Asp Arg Ile Ser
 740 745 750
 Thr Glu Pro Asp Ala Gly Val Met Leu Lys Ile Thr Lys Pro Gly Ile
 755 760 765
 Asn Asp Ala Gly Val Tyr Val Leu Leu Val Arg Leu Asp His Ser Arg
 770 775 780
 Ser Thr Asp Gly Phe Ile Leu Gly Val Asn Val Tyr Thr Ala Gly Ser
 785 790 795 800
 His His Asn Ile His Gly Val Ile Tyr Thr Ser Pro Ser Leu Gln Asn
 805 810 815
 Gly Tyr Ser Thr Arg Ala Leu Phe Gln Gln Ala Arg Leu Cys Asp Leu
 820 825 830
 Pro Ala Thr Pro Lys Gly Ser Gly Thr Ser Leu Phe Gln His Met Leu
 835 840 845
 Asp Leu Arg Ala Gly Lys Ser Leu Glu Asp Asn Pro Trp Leu His Glu
 850 855 860
 Asp Val Val Thr Thr Glu Thr Lys Ser Val Val Lys Glu Gly Ile Glu
 865 870 875 880
 Asn His Val Tyr Pro Thr Asp Met Ser Thr Leu Pro Glu Lys Ser Leu
 885 890 895
 Asn Asp Pro Pro Glu Asn Leu Leu Ile Ile Ile Pro Ile Val Ala Ser

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	900		905		910										
Val	Met	Ile	Leu	Thr	Ala	Met	Val	Ile	Val	Ile	Val	Ile	Ser	Val	Lys
	915						920				925				
Arg	Arg	Arg	Ile	Lys	Lys	His	Pro	Ile	Tyr	Arg	Pro	Asn	Thr	Lys	Thr
	930					935					940				
Arg	Arg	Gly	Ile	Gln	Asn	Ala	Thr	Pro	Glu	Ser	Asp	Val	Met	Leu	Glu
	945				950					955					960
Ala	Ala	Ile	Ala	Gln	Leu	Ala	Thr	Ile	Arg	Glu	Glu	Ser	Pro	Pro	His
				965					970						975
Ser	Val	Val	Asn	Pro	Phe	Val	Lys								
			980												

<210> SEQ ID NO 110
 <211> LENGTH: 2976
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: VZV-gEg1 nucleic acid sequence

<400> SEQUENCE: 110

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aagcttgcca ccatgggaac tgtcaacaaa cctgtcgtcg gcgtgctgat gggcttcggc      60
attattactg gaacactgag aatcacaaat cctgtccggg cctctgtgct gcggtacgac      120
gatttcacac tcgacgaaga taagetggac accaatagtg tgatgagacc ctactatcac      180
tcagatcatg ctgaaagctc ctgggtcaac cgcggggagt ctagtcgaaa agcatacgac      240
cacaacagcc cctatatctg gcctagaaat gactacgatg gatttctgga aaacgcccat      300
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<210> SEQ ID NO 111

<211> LENGTH: 591

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: VZV-gC amino acid sequence

<400> SEQUENCE: 111

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 20             25
Lys Arg Ile Gln Ile Asn Leu Ile Leu Thr Ile Ala Cys Ile Gln Leu
 35             40             45
Ser Thr Glu Ser Gln Pro Thr Pro Val Ser Ile Thr Glu Leu Tyr Thr
 50             55             60
Ser Ala Ala Thr Arg Lys Pro Asp Pro Ala Val Ala Pro Thr Ser Ala
 65             70             75             80
Ala Ser Arg Lys Pro Asp Pro Ala Val Ala Pro Thr Ser Ala Ala Thr
 85             90             95
Arg Lys Pro Asp Pro Ala Val Ala Pro Thr Ser Ala Ala Thr Arg Lys
100            105            110

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Pro	Asp	Pro	Ala	Val	Ala	Pro	Thr	Ser	Ala	Ala	Thr	Arg	Lys	Pro	Asp
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Pro	Ala	Val	Ala	Pro	Thr	Ser	Ala	Ala	Thr	Arg	Lys	Pro	Asp	Pro	Ala
	130					135					140				
Val	Ala	Pro	Thr	Ser	Ala	Ala	Thr	Arg	Lys	Pro	Asp	Pro	Ala	Val	Ala
145					150					155					160
Pro	Thr	Ser	Ala	Ala	Ser	Arg	Lys	Pro	Asp	Pro	Ala	Ala	Asn	Thr	Gln
				165					170					175	
His	Ser	Gln	Pro	Pro	Phe	Leu	Tyr	Glu	Asn	Ile	Gln	Cys	Val	His	Gly
			180					185					190		
Gly	Ile	Gln	Ser	Ile	Pro	Tyr	Phe	His	Thr	Phe	Ile	Met	Pro	Cys	Tyr
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Met	Arg	Leu	Thr	Thr	Gly	Gln	Gln	Ala	Ala	Phe	Lys	Gln	Gln	Gln	Lys
	210					215					220				
Thr	Tyr	Glu	Gln	Tyr	Ser	Leu	Asp	Pro	Glu	Gly	Ser	Asn	Ile	Thr	Arg
225					230					235					240
Trp	Lys	Ser	Leu	Ile	Arg	Pro	Asp	Leu	His	Ile	Glu	Val	Trp	Phe	Thr
				245					250						255
Arg	His	Leu	Ile	Asp	Pro	His	Arg	Gln	Leu	Gly	Asn	Ala	Leu	Ile	Arg
		260						265						270	
Met	Pro	Asp	Leu	Pro	Val	Met	Leu	Tyr	Ser	Asn	Ser	Ala	Asp	Leu	Asn
		275					280						285		
Leu	Ile	Asn	Asn	Pro	Glu	Ile	Phe	Thr	His	Ala	Lys	Glu	Asn	Tyr	Val
	290					295					300				
Ile	Pro	Asp	Val	Lys	Thr	Thr	Ser	Asp	Phe	Ser	Val	Thr	Ile	Leu	Ser
305					310					315					320
Met	Asp	Ala	Thr	Thr	Glu	Gly	Thr	Tyr	Ile	Trp	Arg	Val	Val	Asn	Thr
				325					330						335
Lys	Thr	Lys	Asn	Val	Ile	Ser	Glu	His	Ser	Ile	Thr	Val	Thr	Thr	Tyr
			340					345						350	
Tyr	Arg	Pro	Asn	Ile	Thr	Val	Val	Gly	Asp	Pro	Val	Leu	Thr	Gly	Gln
		355					360						365		
Thr	Tyr	Ala	Ala	Tyr	Cys	Asn	Val	Ser	Lys	Tyr	Tyr	Pro	Pro	His	Ser
	370					375						380			
Val	Arg	Val	Arg	Trp	Thr	Ser	Arg	Phe	Gly	Asn	Ile	Gly	Lys	Asn	Phe
385					390					395					400
Ile	Thr	Asp	Ala	Ile	Gln	Glu	Tyr	Ala	Asn	Gly	Leu	Phe	Ser	Tyr	Val
				405					410						415
Ser	Ala	Val	Arg	Ile	Pro	Gln	Gln	Lys	Gln	Met	Asp	Tyr	Pro	Pro	Pro
			420					425					430		
Ala	Ile	Gln	Cys	Asn	Val	Leu	Trp	Ile	Arg	Asp	Gly	Val	Ser	Asn	Met
	435						440					445			
Lys	Tyr	Ser	Ala	Val	Val	Thr	Pro	Asp	Val	Tyr	Pro	Phe	Pro	Asn	Val
	450					455					460				
Ser	Ile	Gly	Ile	Ile	Asp	Gly	His	Ile	Val	Cys	Thr	Ala	Lys	Cys	Val
465					470					475					480
Pro	Arg	Gly	Val	Val	His	Phe	Val	Trp	Trp	Val	Asn	Asp	Ser	Pro	Ile
				485					490						495
Asn	His	Glu	Asn	Ser	Glu	Ile	Thr	Gly	Val	Cys	Asp	Gln	Asn	Lys	Arg
			500					505						510	
Phe	Val	Asn	Met	Gln	Ser	Ser	Cys	Pro	Thr	Ser	Glu	Leu	Asp	Gly	Pro
		515					520						525		

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Ile Thr Tyr Ser Cys His Leu Asp Gly Tyr Pro Lys Lys Phe Pro Pro
 530 535 540

Phe Ser Ala Val Tyr Thr Tyr Asp Ala Ser Thr Tyr Ala Thr Thr Phe
 545 550 555 560

Ser Val Val Ala Val Ile Ile Gly Val Ile Ser Ile Leu Gly Thr Leu
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Gly Leu Ile Ala Val Ile Ala Thr Leu Cys Ile Arg Cys Cys Ser
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<210> SEQ ID NO 112

<211> LENGTH: 1797

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: VZV-gC nucleic acid sequence

<400> SEQUENCE: 112

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attaacctga tcctgacaat tgccctgtatc cagctgtcaa ccgagagcca gcccacacct   180
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ccaacctcog cagcctctcg aaaacctgat ccagccgtgg ctctacttc cgctgcaacc   300
cgaaagccag accctgcagt ggcaccaaca tctgccgcta ctagaaaacc agatcccgt   360
gtggcaccca ccagtgcagc cacaaggaag cctgaccctg ctgtggetcc tacttctgct   420
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cccgtgtgg caccacaag tgcagcctca cggaaacctg atccagctgc aaacctcag   540
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gccgctttta agcagcagca gaaaacatac gagcagtata gtctggacc tgaagggtca   720
aacatcacc gatggaagtc cctgattcgg ccagacctgc acatogaagt gtggttcaca   780
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cccgtgatgc tgtactctaa cagtgcgat ctgaatctga ttaacaatcc tgagatcttc   900
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gccactacct tcagtggtggt cgccgtgatc attggcggtca tctctattct ggggaccctg 1740

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<210> SEQ ID NO 113

<211> LENGTH: 340

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: VZV-gK amino acid sequence

<400> SEQUENCE: 113

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35 40 45Val Val Trp Gly Ser Tyr Asn Asn Ser Leu Ile Tyr Val Thr Phe Val
50 55 60Asn His Ser Thr Phe Leu Asp Gly Leu Ser Gly Tyr Asp Tyr Ser Cys
65 70 75 80Arg Glu Asn Leu Leu Ser Gly Asp Thr Met Val Lys Thr Ala Ile Ser
85 90 95Thr Pro Leu His Asp Lys Ile Arg Ile Val Leu Gly Thr Arg Asn Cys
100 105 110His Ala Tyr Phe Trp Cys Val Gln Leu Lys Met Ile Phe Phe Ala Trp
115 120 125Phe Val Tyr Gly Met Tyr Leu Gln Phe Arg Arg Ile Arg Arg Met Phe
130 135 140Gly Pro Phe Arg Ser Ser Cys Glu Leu Ile Ser Pro Thr Ser Tyr Ser
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165 170 175Tyr Thr Lys Leu Ala Arg Leu Leu Cys Asp Val Ser Met Arg Arg Asp
180 185 190Gly Met Ser Lys Val Phe Asn Ala Asp Pro Ile Ser Phe Leu Tyr Met
195 200 205His Lys Gly Val Thr Leu Leu Met Leu Leu Glu Val Ile Ala His Ile
210 215 220Ser Ser Gly Cys Ile Val Leu Leu Thr Leu Gly Val Ala Tyr Thr Pro
225 230 235 240Cys Ala Leu Leu Tyr Pro Thr Tyr Ile Arg Ile Leu Ala Trp Val Val
245 250 255Val Cys Thr Leu Ala Ile Val Glu Leu Ile Ser Tyr Val Arg Pro Lys
260 265 270Pro Thr Lys Asp Asn His Leu Asn His Ile Asn Thr Gly Gly Ile Arg
275 280 285Gly Ile Cys Thr Thr Cys Cys Ala Thr Val Met Ser Gly Leu Ala Ile
290 295 300Lys Cys Phe Tyr Ile Val Ile Phe Ala Ile Ala Val Val Ile Phe Met
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340

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<210> SEQ ID NO 114
<211> LENGTH: 1044
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: VZV-gK nucleic acid sequence

<400> SEQUENCE: 114

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tctcagaaac attgataact cgag                                          1044

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- The invention claimed is:
1. A nucleic acid molecule comprising a coding sequence for a herpes virus antigen encoding one or more proteins selected from the group consisting of:
 - a protein comprising VZV-gH (N-terminal region up to position 841 of SEQ ID NO:99);
 - a protein comprising VZV-gL (C-terminal region from position 849 of SEQ ID NO:99);
 - a protein comprising VZV-gE (N-terminal region up to position 623 of SEQ ID NO:109);
 - a protein comprising VZV-gI (C-terminal region from position 631 of SEQ ID NO:109); and
 - a protein comprising SEQ ID NO:111.
 2. The nucleic acid molecule of claim 1, wherein the nucleic acid molecule further comprises an additional nucleotide sequence that encodes a different herpes virus antigen selected from the group consisting of: HCMV gB, HCMV gM, HCMV gN, HCMV gH, HCMV gL, HCMV gO, HCMV-UL131a, HCMV-UL130, HCMV-UL128, HCMV-UL83, HSV1-gB, HSV1-gH, HSV1-gL, HSV1-gC, HSV1-gD, HSV2-gB, HSV2-gH, HSV2-gL, HSV2-gC, HSV2-gD, VZV-gB, VZV-gH, VZV-gL, VZV-gM, VZV-gN, VZV-gE, VZV-gI, VZV-gC, VZV-gK, CeHV1-gB, CeHV1-gH, CeHV1-gL, CeHV1-gC, and CeHV1-gD.
 3. A nucleic acid molecule comprising a coding sequence for a herpes virus antigen selected from the group consisting of:
 - a nucleotide sequence comprising SEQ ID NO:98; a nucleotide sequence that is at least 95% homologous to SEQ ID NO:98;
 - a nucleotide sequence comprising nucleotides 13-2535 of SEQ ID NO:100, encoding VZV-gH; a nucleotide sequence that is at least 95% homologous to nucleotides 13-2535 of SEQ ID NO:100, encoding VZV-gH;
 - a nucleotide sequence comprising nucleotides 2557-3033 of SEQ ID NO:100, encoding VZV-gL; a nucleotide sequence that is at least 95% homologous to nucleotides 2557-3033 of SEQ ID NO:100, encoding VZV-gL;
 - a nucleotide sequence comprising nucleotides 13-1317 of SEQ ID NO:102, encoding VZV-gM; a nucleotide sequence that is at least 95% homologous to nucleotides 13-1317 of SEQ ID NO:102, encoding VZV-gM;
 - a nucleotide sequence comprising nucleotides 1339-1599 of SEQ ID NO:102, encoding VZV-gN; a nucleotide sequence that is at least 95% homologous to nucleotides 1339-1599 of SEQ ID NO:102, encoding VZV-gN;
 - a nucleotide sequence comprising nucleotides 13-1881 of SEQ ID NO:110, encoding VZV-gE; a nucleotide sequence that is at least 95% homologous to nucleotides 13-1881 of SEQ ID NO:110, encoding VZV-gE;
 - a nucleotide sequence comprising nucleotides 1903-2964 of SEQ ID NO:110, encoding VZV-gI; a nucleotide

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sequence that is at least 95% homologous to nucleotides 1903-2964 of SEQ ID NO:110, encoding VZV-gI; a nucleotide sequence comprising SEQ ID NO:112; a nucleotide sequence that is at least 95% homologous to SEQ ID NO:112;

a nucleotide sequence comprising SEQ ID NO:114; and a nucleotide sequence that is at least 95% homologous to SEQ ID NO:114.

4. The nucleic acid molecule of claim 3, comprising one or more nucleotide sequences selected from the group consisting of: SEQ ID NO:98; a nucleotide sequence comprising nucleotides 13-2535 of SEQ ID NO:100, encoding VZV-gH; a nucleotide sequence comprising nucleotides 2557-3033 of SEQ ID NO:100, encoding VZV-gL; a nucleotide sequence comprising nucleotides 13-1317 of SEQ ID NO:102, encoding VZV-gM; a nucleotide sequence comprising nucleotides 1339-1599 of SEQ ID NO:102, encoding VZV-gN a nucleotide sequence comprising nucleotides 13-1881 of SEQ ID NO:110, encoding VZV-gE; a nucleotide sequence comprising nucleotides 1903-2964 of SEQ ID NO:110, encoding VZV-gI; SEQ ID NO:112; and SEQ ID NO:114.

5. The nucleic acid molecule of claim 4, wherein the nucleic acid molecule is a DNA plasmid.

6. The nucleic acid molecule of claim 3, wherein the nucleic acid molecule further comprises an additional nucleotide sequence that encodes a different herpes virus antigen selected from the group consisting of: HCMV gB, HCMV gM, HCMV gN, HCMV gH, HCMV gL, HCMV gO, HCMV-UL131a, HCMV-UL130, HCMV-UL128, HCMV-UL83, HSV1-gB, HSV1-gH, HSV1-gL, HSV1-gC, HSV1-gD, HSV2-gB, HSV2-gH, HSV2-gL, HSV2-gC, HSV2-gD, VZV-gB, VZV-gH, VZV-gL, VZV-gM, VZV-gN, VZV-gE, VZV-gI, VZV-gC, VZV-gK, CeHV1-gB, CeHV1-gH, CeHV1-gL, CeHV1-gC, and CeHV1-gD.

7. The nucleic acid molecule of claim 6, wherein the nucleic acid molecule comprises a coding sequence for a VZV antigen, and wherein the additional nucleotide sequence encodes a herpes virus antigen selected from VZV-gB, VZV-gH, VZV-gL, VZV-gM, VZV-gN, VZV-gE, VZV-gI, VZV-gC, or VZV-gK.

8. The nucleic acid molecule of claim 3, wherein the nucleic acid molecule is a plasmid.

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9. The nucleic acid molecule of claim 3, wherein the nucleic acid molecule is an expression vector, and the coding sequence is operably linked to regulatory elements.

10. The nucleic acid molecule of claim 3, wherein the nucleic acid molecule is incorporated into a viral particle.

11. A composition comprising one or more nucleic acid molecules of claim 3.

12. A method of inducing an immune response against a herpes virus antigen comprising administering a nucleic acid molecule of claim 3 to an individual.

13. A method of protecting an individual from herpes virus infection comprising administering a nucleic acid molecule of claim 3 to an individual.

14. A method of protecting an individual who has been diagnosed with herpes virus infection comprising administering a nucleic acid molecule of claim 3 to an individual.

15. A protein selected from the group consisting of:

a protein comprising VZV-gH (N-terminal region up to position 841 of SEQ ID NO:99);

a protein comprising VZV-gL (C-terminal region from position 849 of SEQ ID NO:99);

a protein comprising VZV-gE (N-terminal region up to position 623 of SEQ ID NO:109);

a protein comprising VZV-gI (C-terminal region from position 631 of SEQ ID NO:109); and

a protein comprising SEQ ID NO:111.

16. A method of inducing an immune response against a herpes virus infection comprising delivering to an individual a protein of claim 15.

17. A method of treating an individual who has been diagnosed with herpes virus infection comprising delivering to said individual a protein of claim 15.

18. The nucleic acid molecule of claim 1, wherein the nucleic acid molecule is a plasmid.

19. The nucleic acid molecule of claim 1, wherein the nucleic acid molecule is an expression vector, and the coding sequences encoding said one or more proteins are operably linked to regulatory elements.

20. A composition comprising a nucleic acid molecule of claim 1.

* * * * *